

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGA
CCACCGCGTCGGGCGGAGCAGCACGCCGAGGACCTGGAGCTCCGGCTCGCTTCCG
CAGCGCTACCCGCCATCGCCTGCCGCCGGCGCTGGGCTCCTGCCGTTCTGCTG
CTGCTGCCGCCGCCGCCGGAGGCCAAAGGCCAGGCCAACCGCAAAGAACCTTGCGGCCGGAAACA
CGGCTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCCAGAGCAGCGACTCGAATGCAATCAGATGCTAGAGGCCAGGAGGA
GCACCTGGAGGCCCTGGCTGCCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTCTCCAGGAACCTACGGTCCCAGTGTCTGCATGC
CAGGGCGGATCCCAGAGGCCCTGCCAGCGGAATGCCACTGCCAGGGAGATGGGAGCAGACA
GGGCAGCGGCTCTGCCGTGCCACATGGGGTACCAAGGGCCGCTGTGCAGTGCATGG
ACGGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATGCAAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCCTGACCAACAGAGACTGCCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGGCCCTGTGATGTGGACGAGTGTGGCCGAGGCCCTCCCTGCAGCGCTG
CCGAGTCTGTAAGAACGCCAACGGCTCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGAAAGGCCAGGAACCTGTAAAGAGTGTATCTCTGGCTACGGAGGGAGCA
CCGACAGTGTGCAAGATGTGACGAGTGTCACTAGCAGAAAAACCTGTGAGGGAAACG
AAAATGCTACAATACTCCAGGGAGCTACGCTGTGTCCTGACGGCTTCCAAGAAACG
GAAGATGCCCTGTGCCGCCAGGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCAAGACCTGTAAATGTGCCGACTTACCCCTAAATTATTCAAGAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGCTCTGCAGTGGACAGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGCCCTTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATAACAGTTCTTGTAAATAAAATTGACCATTGAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAGGCCGCCGCACTCTAGAGTCGACCTGCAGAAC
TTGGCCGCCATGCCCAACTTGTATTGAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTCAAAATAAGCATTTTCACTGCATTCTAGTTGTGGTTGTCACAAACTC
ATCAATGTATCTTATCATGCTGGATCGGAATTAACTGCCGAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCCAGAACCTGAGCTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCAGGCTCCCCAGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWCVKTLKVCCSPGTYGPDCLACQGGSQRPCSNGHC
SGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCCKTCGLTNRDCCCEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAATGCACCTCGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGTCCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAACCGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGAGTATCTGACGGCCAGGTTGCGTAGGTGCG
GCACGAGGACTTCCCGGAGCGCAGGAGCTGCAGCATGCCCGGAGGAGCGCCCTTC
CCTGCGCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCAGGAGGC
CGGGCCGCCAGGAGGAGCCTGACTATGGATCGATGCTACCAGGCAAGAGTACTCA
TAGGATTGAAAGAAGATATCTGATTGTTCAAGGGGAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAACATGCCAGTATTCTGTAATCATCCATTGAAATTTC
CTGGCAAGCTGCAGGGCAGGAGAACATCTATGAATTCTGCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGTGCCTCACAGGCA
TCAGTGTTCAGTTGGTTCCCATGCTTGAAAACAGGATGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAAATTCTGAAGGCACACCATCTCCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAAGCTGAGTGCAGGCCAGGGCGGAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAAGGGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCATTG
TACCCACGATGTATGAATTGGGACTTTGTGTGACTCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACACTGCTCAACCCACCTGCTTTAATGGAGGGACC
TGTTCACCTGGAAAATGTTATTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAAGGCCAACACCTCTGCAATGGAGGTAATGCAATTGTTAAAGCAAATGTAAGTGT
CCAAAGGTTACAGGGAGACCTCTGTCAAAGCTGCTGAGCTGGCTGTGCAACAT
GGAACCTGCCATGAAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAAGGCCAGCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACAGCCTTCACTTAAAGGCCAGGAGGCCGGGACTGCAATCCAAATACATCTGG
TGAACCTCGACATCTGAAACGTTTAAAGTTACACCAAGTTCAAGGCTTTGTTAACCTTCA
TGTGTTGAATGTTCAAATAATGTCATTACACTTAAGAAATACTGGGCTGAAATTAGCT
TCATTATAAAATCACTGAGCTGATATTCTCTTCAAGTTCTAAGTACGTCTGAG
CATGATGGTATAGATTTCTGTTCTGCTTCAAGTGGGACAGATTATATTATGTCATTGAA
TCAGGTTAAAATTTCACTGTTGAGTTGGCAGATATTCTAAAATACATGCAATTATGTT
GTCGGGGGGAGGGGAACATCAGAAAGGTTAAATGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTCAGATATTAGAT
GTTGTTACATTAAAATGCTCTTAATTAAACTCTCAATACAATATTGACCTT
TTACCAATTTCAGAGATTCACTGTTGAGTTAAAACACATGCAATTGTCATTG
AAACAATATAATATATTCTAAACACAATGAAATAGGAAATATAATGTAACCTTGCAT
TGGCTGAAAGCAATATAATATTGTAACAAAACACAGCTTCACTAAACATT
ACTGTTGTTGATGTATAAAATAAGGTGCTGTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTATTGCACTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAAQRMPAIPVNIHSMNFTWQAAGQAELYFELSLRSLDKGIMADPTVNVPOLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFNCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICCPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCGGCGGTGCAGAGCCAGGAGGCGGAGGCCGCCGGCCAGCCTGGG
CCCCAGCCCACACCTTCAACAGGGCCAGGAGCACCATGTTGGCGATGTCACCTGGGCTAC
TGCTGTTGCTGGCGTGGCTGGCACTTGGCTCTGGGTGCCAGCAGGGCTGGGCGCCGG
GAGCTAGCACGGGTCTGCACCTGGGGGATCGGGGACGGGGAGGCCGACTGCCAGGA
GCAGGACCTGTGCTGCCGGCGGTGCGACACTGTCGCTTACCTGGGCCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCGACTGTCGCTTACCTCTGGGACTTC
TGCCTGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTGATCTA
TCCAGGTCTGGGAAACGTAACGGACTGTAACCGTGTGCACTGCCAGGAGAACAGGAGT
GGCATGGTGGATCAGACATGCAACAGGCCAACATGGCTGGCAGGGTGG
GAACACAGCGCCCTCTGGGCATGACCTGGATGAGGGCACTATGGCTGGCAGGGTGG
TCCGCCATCTTCTCGGTATGAAATTTATACAGTGTGAAACCAGGGAG
GTGCTTCCACAGCCTTCGAGGCCCTGTAGAAGTGGCCCAACCTGATTGATGAGCCTTGTGA
CCAAGGCAACTGTGAGGCCCTGGCCCTCTCCACAGCAGCTGTGGCATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTGTCGCCCCAGAACCTGCTGTCTTGGA
ACCCACAGCAGCAGGGCTGGGGCTGGGCTCTCGATGGCTGTGTCGCCCC
CCGAGGGGTGGTGTGCAACTGCTACCCCTCTCGGGCCGTGAAAGAGCAGGGCTGCC
CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGCTGGGGCAAGGCCAGGGCACTGCC
CACTGTCCCCAACAGCTATGTAATAACATGACATCTACCAAGGTCACTCTGTCTACCGCC
CGGCTCAACAGCAAGGAGATCATGAGGGAGCTGTGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGATGAGGACTCTTCTATAACAGGGAGGCACTACAGGCCACAGCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCAACTCAGTAAGATCACAGGATGGG
AGAGGAGACGCTGCCAGATGGAAGGAGCCTCAAAATACTGGACTCGGGCAACTCTGGGCC
CAGCCCTGGGCGAGGGGCCACTTCCGCATCGTGCAGGGCTCAATGAGTGCAGATCGAG
AGCTTCTGTCTGGCGCTCTGGGCGCTGGGAGGACATGGGTATCAACTGAGGCTG
GGGGCACCACGGGGCTGGGCTGGGATCAGGCTAAGGGCGGGAGAGGCCCAATG
GGGCGGTGACCCCGACGGCTCGCCGCAGAGCCCCGGGGCAGGGGGCGCAGGGCGCTAAT
CCCGGCGGGGTTCCGCTGACGCAAGCGCCCGCTGGGAGGCCAGGGAGACTGGCG
GAGCCCCCAGACCTCCCACTGGGAGGGGGCAGGGCCTGGGAGAGCAAGCTGCAG
ATCCCCAGGCCCTGGGCCCAACTCAAGACTACAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCCAACCCCACTCCGTTATCTTTTTTTTTTTAGACAGGGCTTGTCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACTCCGCTACCTGGG
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGG
TAATTTTTGTATTTTTGTAAAGAGGGGGTCTACTGTGTTGCCAGGCTGGTTTCAACT
CTGGCTCAAGCGGTCCACCTGCCTCCCTCCAAAGTGTGAGGATTGCACTGAGG
ACTGCAACCCAGGCCCTGTATCTTATTCTTCAAGATATTATTTCTTTCAGTGTAAAA
AAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHIALGAQQGRGRRELAPGLHLRGIR DAGG RY CQE QDLCCRGRADDC
ALPYLGAIC YCDLFCNRTVSDCCPDFWDFCLGVPPPFPPIQGCMHGGRIYPVLGYWDNCNR
CTCQE NRQWHGGSRHDQSHQPGQLWLAGWE PQRLLGHD P G
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCGTCTGCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGCGTCTCGATGGTGCCTGGTGGTTCCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCGGGCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGGAGCTGATGGAGAAATGGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGATGCCTGCAGGTGGAGAATGCACCCAGCTGGGG
GAGCAGTGCTGGACCCGCCATCCGCGCAGTGGCCCTGCACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGCAACGCCAGCGGGCCCATGCCCTGCAGCCGGCTGCCCATCCTT
GCCGCTGCCCTGCACTCGGCTGCTCTGGGACCCGGCAGTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCTCTGTGCCACTCCTCACAGACTG
GCCCAGGTGGGAGCCTGTCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCTGAGATGGCCCTCCAACCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGCGTGGTCCCCCGACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGGCTGGAGGCTGGAGGAA
GGGGCCAGGCCTCACATTCGTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DP PADGPSNPLCCCFHGPASFSTLN PVLRLHLPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACCGCGTCCGAACCTCTCCAGCGATGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTCAACGGCGTCGCATCTCCGCCACCGCGAGGACGGAAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAAACTATAACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGGCAGGGCGGCCAGGCTCCCGCAGCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAAGCAGAACAGCTCGAGTTGTGGCTCCGCCACCCCGGACCAAGCGCACAC
GGCGGCCAGCCCTCAGCTAGTCTGGAGGCAGGGGGCAGCAGCCCTGGCCGCCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCTTCCGGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGCAAGACAACCGTCTGGAGGTGGCTGTCCCTCAAA
TCTGCTTCTCGATCTCCCTCAGTCTGCCCTCAGGCCACCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCAACTCCAGCCC
CGGAATAAAACCA~~TTT~~CCTGC

FIGURE 11

MGAARLLPNLTLCLOLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHKVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNNKRGKLIGKPSGKSKDGVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGOLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCACATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCAGACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCCTAGCTGGAGTTCTGGACTTCACAGAACCCCATCCAGT
CATTTGATTTGCTGTTTATTTTTCTTTTCTTTCCACCCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGCCTACAGACCAAAAGTGGCCAGGCATGGGCTTTTCCCT
GAAGTCTTGGCTTATCATTCCCTGGGCTACTCACAGGTGTCAAACCTCTGGCTGCC
CTAGTGTGTCGCCGCTGCGACAGGAACCTTGTCTACTGTAACTGAGCGAAGCTTGACCTCAGT
CCTCTTGGGATCCCGGAGGGCTAACCGTACTCTACCTCCACAAACACAAATTAAATG
TGGATTTCCTGAGAACCTGACAATGTACAGTCGGTGCACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCAAGAAATGTACAGAGTTCCATTGAGGAAAC
AATATTGAGAACCTTACCGGCTGCTTGTGCCAGCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCATATCCACAGTGGGGTGAAGACGGGCTTCCGGGAGGCTATTAGGC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCACATGGCTTCCAGAA
TCTCACGAGCTGGAGCGTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGGACATCTACCAAGCTCAAGGAATTTCATTGTAAGTACGTAATTGCTGTCC
CACCCCTCCCTCCGATCTCCAGGTACGATCTGATCAGGCTTATTTGCAAGGAAACCCAGAT
AAACACATTCCCTTGAACGGCTTCTCAAAATCTCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTGATAATCTCTCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTTGTGTTTGTGACTGAGTATTAAATGGTCACAGAAATGGCTCAA
ATATATCCCTCATCTCTCACAGTCGGGGGTTTGTGCAAGGCTCTGAAACAAGTCCGGG
GGATGGCCGTAGGGAATTAAATGAAATTCTTGTCTGTGCCCCACAGCACCCCCGGCTG
CCTCTTCTCACCCCCAGCCCCAGTACAGCTTCTCGACCAACTCAGCTCCACCCCTCTAT
TCCAAACCCTAGCAGAACGCTACAGCCTCCAACCTTACACATCGAAACTTCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGAACCCCACCTATTCTGAACGGATCAGCTCTATC
CATTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCACCCTGATGGCATA
CAAATCACATGGGTGAAAATGGGCCACAGTTAGTAGGGGGCATCGTTAGGGCGCATAG
TCAGCGGTGAGAAGCAACACTGAGCTGGTTAACTTAGAGCCCCGATCCACCTATGGATT
TGTGTTAGTGCCTACTGGATGCTTTAACTACCGCGCGTAGAAGACACCATTGTTAGAGGC
CACACCCATGCCCTATCTGAACACAAGGGCAGCAACACAGCTCAGCCATGAGCAGACGA
CGTCCCCACAGCATGGGCTCCCCCTTCTGTCGGGGCTTGATGGGGGGCGGGTGTATATT
GTGCTGGTGGCTTGTCTAGCGTCTTTGCTGGCATATGCAAAAAGGGGGCTACACCTC
CCAGAAGTGGAAATAACAACCGGGGCCGGGAAAGATGATTATGCGAGGGCAGGCCACCAAGA
AGGACAACCTCATCTGGAGATGACAGAAACAGTTCTAGATGCTCTCTTAATAACGAT
CAACTCCCTAAAGGAGATTCTAGACTGCAAGCCATTACACCCCAATGGGGGCTTAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGGGCCAGGCTTATCAAGGGGAAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACACGAGATTACATTGATAATGGATTAAAAAAAGTG
TTGTGCAATTGATAACTCTGTAATTATAAGGTGACTATATAATGGATTAAAAAAAGTG
CTATCTTCTATTTCAAGTAAATTACAAACAGTTTGTAACTCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPSPHGAAFFLKSWSLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLVLYLHNNOINNAGFPAELHNQSVHTVYLYGNQLDEFPMNLPKNVRVLH1QENNIQTI
SRAALAQLLKLEELHLDNSI STVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRRIAVISDMAFQNLTSLERLIVDGMLLTNKGIAEGTFSHLLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYIQDNQINH1PLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARVELNMNLLSCPPTTPGLPLFTP
APSTASPTTQPPTLSIPNPNPSRSYTPTPTSKLPTIPDWDRGERVTTPPISERIQLSIHFVNND
TSIQVSWLSSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVLVPL
DAFNYRAVEDITCSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVVLVVVL
LSVFCWHMHKKGRYTSQWKYNRGRKDDYCEAGTKKDNSILEMTE TSFQIVSLNNNDQLLKG
DFRLQPIYTPNGGINYTDCHI PNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCGGCGGCGGAGACAGAGGCAGAGGCCAGAAGCTGGGGCTCCGCTCGCCCTCCACGAGGC
ATCCCCGAGGAGGCCCGGCGCTCGCAGGCCCTTGCTGCCCTCTGCTGCCCTGAAATGGAAAAGATGCTCGCAGGCT
TCGCTTCCCAGGGCCGCGCTGAGGCCCTCTGCTGCCCTGAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTGCCAGACATGCTCCCTCCCTGCCAGGGAGCGGTACCGTGGAGGGTCCATCT
CTAGGGAGAGCACGCTGCCAGGCCACCCGCCAGAGGCCCTTGAGAGTTCTGTGAGAACAAAGCCGAGAC
TGGTTTCATCATGAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGGAGTTCATGTTGACA
TCTTGCAATTCTTGGACATTGGCTCTGATGTCAGCTGCCCTGCTGAAATATGGCAGCAGCTGTCAGAAATG
AGTTCTCCCTAAGACCTTAAGAGGAAGCTGGAGGTGGAGCTGCTGTCAGAAGGGATGCCGATCTGTCACCG
GCACCATGACTGCGCTGCCATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGAGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGCTATAATGATGTCAGAGCTGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCCACGGGACACGGGCTATAATTTGGCATGGTGGCCAGGTGACTTAAACACCTTGAAAGTCCATTG
GGAGTGGGCCCATGGAGGACCATGTCCTTGTGGCCAATTTCAGGAGATGAGCGCTGACCTCCGTTC
AGAGAGAAGTTGTGACGGGCCCATAGTCAGCAGCACCCTGCTGAGCTACTTCTGCTCATCAACATCCCTG
GCTCATAGCTGCTGAGGTCAAACAGGCTACATTCTCAACTCGGATCAGACCACTGCAAGATCCAGGATCTG
GTGCGCATGGAGGACACAAACTGTGAGCAGCTGTCAGTGAATGTCGGGCTCCTCTGCTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGTGTGTCGGCTGGACTACTGTGCTCAGAAAACCAACGGATGTGAAAC
ATGAGTGTGAAATGCTGATGCTCTTACCTTGGCATGGTGGAGCTTGTGCTTAAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTGTGCACTGAAACAAACGGGCTGTGAGCATGAGTGGCTAACATGEGAGGAGAGCT
ACTACTGGCTGCTGCCACGGCTGCTACACTCTGGACCCAACTGGCAGGCTGAGCTGGGACCAACTGTGCAAC
AGCAGGACCATGCGTGTGACCGAGCTGTGTCACACCGAGGATTCCTCTGCTGCAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTCTGCCGGGGTGGATTACTGCTCTGAGTGAACATGGTTGTAATACTCCT
GTGTCACATGGACAGATTTGGCTCTGGCTGAGTGGCTCTGGAGGACAGCTGGCTCTCCAGGGATGGGAAGACGTG
CAAATTTGGACTCTTGTGCTGGGGACCCAGGTTGTAACATTCTGTTGTAAGAGTGTGTTGTTGTT
GCCAGTGGCTTGAAGGTTATAACTCCGTGAAGTGGAAAAACCTGAGAAGGAAAGATGCTGCCAAGCTATAG
ACATGCTGTCGAACACATTGTGTAACAGTGCAGCAGCTACACTACAGCTGGAGTGGCTGGAGGGATTCCCGGCT
CTGAGGATGGGAAACGCTGCCAGGAAGGAGATCTGCAAATCAACCCACCATGGTGTGCAACACATTGTGTTA
ATAATGGAAATTCCTACATCTGCAATGTCAGGGGATTGTTACTGCTGAGGAGGGAAGACGGTGAAGAAAT
GCAGTCAAGGCCAACCTGGCTGTGAGTGGATCAAGGACTTGTGAGGAGAAGAAATTGGAGGTG
TGAAGCAGTTGCACTGGAAATTAGATTCTTGTGACATTTCCTCCAAAAGCCGCTGACTGGGCTGCTCCAGT
ATTCCACACAGGTCACACAGAGTCTACTGAGAAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCC
ACATGAAATACATGGGAAAGGCTCTATGCTGGGCTGAGCAGCACCATTGTGTTACCGAGGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGTGCCAGAGCAGCCATTGTGTTACCGAGGAGCAGGCCCTAGGATG
ACGTCTCCGAGTGGCCAGCTAAAGGCCAAAGGCAATGGTACTACTATGCTATGCTGTTGGGTAGGAAAAGCCATTG
AGGAGGAACACTAACAGAGATTTGCTCTGAGGCCAACAAACAGACATCTTCTATGCCAGAAGACTTCAGCACAAATGG
ATGAGATAACTGAAAACCTAACAGAACAGGATCTGTGAGGCTCTAGAAGACTCTGGAGAGCAGGACTCTCCAG
CAGGGGAACGCTGCCAAACAGGTCACAGGCCAACAGAAATCTGAGGAGCAGTACCCATTAAATATCCAAGACCTACTTT
CCTGTTCTAATTTCAGTGCACACAGATCTGTTGAGAAGGAAACATTTTACGGTCTACACAAAAGCTT
CCCATTCACAAACACCTTCAGGAAGGCCCTTGGAGAAAAAACAGCATCAATGCAAAATGTAACACCTTATAATG
TCCAGAACCTTGCAAAAGGAAGAACTAAGAAAATTAAACACAGGCCCTAGAAGAAAATGACACAGAGAATGGAGGCC
TGGAAATGCCCTGAGATACAGATGAAGATTGAGAACATGGCAGACACATTGTTAGTGTATTGATTCAGGATTACAAT
GAACGCCAGTGCAGGCCAAAGCTCAGGCTTATGTTAAATCAATAATGTTGAGTAAACAAATCAGTACTGA
GAAACCTGGTTGCAACAGAACAAAGACAAGAAGTATACACTAAGCTTGTGAGTAAATTTATCTAGGAAAAAAATCCT
TCAGAAATTCTAAGATGAAATTACAGGTGAGAATGAAATGCTGCAAGGTTTGTGAAATATACTGTGGACAC
AACTGCTTCTGCCATCTGCCCTAGTGTGCACTCTCATTGACTATACGATAAAGTTGCACTGTTACT
CTGAGAACACTGGCCATAGGAATGCTGTTTTTGACTGGACTTTACCTTGATATGATATGATATGGATGTATG
CATAAAATCATAGGACATATGACTCTGGAACAAAGTGGATTTTTACATATAATTAAATTCACCACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRGHARTHPTQTALESCENKRADLVFI
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTGVLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAI VGQVDFN T LKSIGSEPHEDH VFLVANFSQIETLT SVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTT CRI QDLCAMEDHNCEQLCVNPGSFVCQCYSGYA
LAEDGKRCVADYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQQLCLNTEDSFVCQCSEGFLI
NEDLTKCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGTCAKLDS CALGDHGCE
HSCVSSEDSFVCQC FEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVC KSTHHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGII DS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKAVA
HMKYMGMGKGSMTGLALKHM FERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELOEITASEPTNKHLFYAEADFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPV TINI QD LLS CSNFAVQHRYL FEEDNL RSTQKL SHSTKPSGSPL
EEKHDQCKCENLIMFQNL ANEE VRKL TORL EEMTQR MEALE NRL RYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCAGCCTCG
GCACCTGCGAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGCTCCGGCAAGGGAGGGC
CATGATTTCCTCCCCGGGCCCCCTGGTGACCCAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGGGGCCAGCTGCAACTGCACTTGCCCACCCGGTGCAG
GGCGTGGAGGGAGGGAAAGTGGTCTCCAGCGTGGTACACCTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCATCACATCAATGGGTCAACAAGCAAACCTGGAGTATCCTGGTACTCC
ATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAACCT
TAGAACTCAATGTA
CTGGTCTCCAGCTCCTCCATCCTGCCGCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAGGAGTAAGCCGCTGTC
ATACCA
GTGGGATCGGCAGCTTCCATCCTTCAGACTTTCTTGACCCAGCATTAGATGTC
ATCCGTG
GGTCTTAAGCCTACCAACCTTCTGTTCCATGGCTGGAGTCTATGTC
TCAAGGGCCAC
AATGAGGTGGGACTGCCAATGTA
ATGTGACGCTGGAAGTGA
GACAGCACAGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCTGGTTGGACTGGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCAATGATATCAAGGAGGATG
CC
ATTGCTCCCCGACCTGCCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCCTGTCACTCCGCAGGCCCTCGGCCACCCATGGCCCTCCAGGCC
TGACCCCCACGCCAGTCTCAGGCCAGGCCCTGCCCTACCAAGACTGCC
CACAGAT
GGGGCCCACCCCAACCAATATCCCCCATCCCTGGTGGGTTCTCTG
CTGGCTTGAGCC
CATGGGTGCTGTGCTGTGATGGTGCCTGCCAGAGTC
AAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGCTCTCCTTCTATAAGGTCACCTCTAGC
AGAGGCCTGAGTC
ATGGGAAAGAGTC
ACACTCTGACCCCTTAGTACTCTGCC
CCCCACCTCT
TTTACTGTGGAAAACC
ATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGAA
TTGGAGGAGGCC
CTCCACCCACCC
CTGACTC
CTCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACT
ACCAAGAGTGAGGGCAGAGACTTCCAGTC
ACTGAGTC
CTCCAGG
CCCC
CTGATCTG
ACCC
ACCC
CTATCA
ACACC
ACCC
CTGGCT
CCACT
CCAGCT
CCCTGT
ATTGATATAACCTGT
CAGGCTGGCTGGTTAGGTTTACTGGGG
CAGAGGATAGGA
ATCTC
TTATTAAA
ACTAAC
ATGAA
ATATGTG
TTTC
ATTGCAA
ATTAA
ATAAG
ATA
ACATAA
TGTTG
TATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPLANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSSLTNLSSMAGVYVCKAHNEVGTAQCNVTLLEVSTGPGAA
VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKEADAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPHPGPPRPGALTPPSLSSQALPSPRLPTTDGAHPQPISPPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGGGCCACCGCCAATGAAACGCCTCCGCTCTAGGGTTTCCACTTTG
TTGAATTGTTCTATACTCAAATTGCAACAGACACCTTGCTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATGCAACATGGGATTTAGGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAATTAACTCAGTCCTGTGGCAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATGTATGTGTACACTGGCTTCAGATCCAGCACTAACCA
AGACAGGTTTATCACTAATGATGAAACCGTCTGTATAGAAAATGTGAATGCAAACGTGCCATT
TAGATAATGTCTGTATAGCTGCAAATTAATTAATAAAATCTGTGGCAGACATCTTCACCAACAGA
GAACCTGTGGCTTGCTACAAGAAGCTATAGAAAATCTGTGGCAGACATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTTCAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACACTCAACTCTACTGAATTGTAACCGCTGAAT
AATTGTTCAAGGGATACTTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAATTCACCGGATATAGCTCCTCAAAGTTTCTTTTGAT
TCATATAACATGAAACATATTCTCATATGGAATATGGATGGAGACTACATAAATATTA
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTGCATTTTATATTATA
AGAGTATTGGTCTTGTCTTGCATCATCTGACAACCTCTTATTGAAACCTCAAACATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCACTTCTCAGTAACTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAAACTTGAACATTTACATTACAAAGTCACTGAAAGGTACACAGATA
GGTATAGGAGTCTATGTGCTATTGAAATTACTCACCTGATACCATGAAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCTTCCATTGGTATTAAAGATTATAATATTCT
TTACAAGGATCACTTAACTAGGAATAATTATTACTGATTTGCTTGCCATATGCACTT
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAAATTCAACAAAATCTTGCTG
TAGCCTATTCTGCTGAACCTGTTTCTTGTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATGCGGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGGGTCATCTACAACAGGGATTGTC
CAAGAATTTTATATGTTGGCTATCTAAGCCCAGCGGGTAGTTGGATTTTGGCAGCAC
TAGGATACAGATAATTGCGACAACCAAAAGTATGTTGGCTTAGCAGGAAACAACTTTATT
TGGAGTTTATAGGACAGCATGCTTAATCATTCTGTTAATCTCTGGTTGGAGTCAT
CATATACAACAGTTTCTGTCACACTGCGGGTTGAAACCAAGAGTTAGTTGCTTGAGAAC
TAAGGTCTGTGCAAGAGGGAGCCCTCGCTCTCTGTTCTCTGGCACCACCTGGATCTT
GGGGTTCTCCATGTTGTCAGCGCATCAGTGGTTACAGCTTACACTCTTCAGTCAGCAATGC
TTTCCAGGGGATGTTCATTTTATTCTGTGTTTATCTAGAAAGATTCAAGAACAGAAT
ATTACAGATTGTCAAAATGCCCCGTGTTGGATGTTAAAGGTAACATAGAGAAC
GTGATAATTCAACACTGCACAAAATTTCAAGCTGTTGGATGCAATGTATAAAA
TGACTCATCAAATTATCAAATTAACTACTAGACAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACCTGATATAAGGTTAAATTATGTTGATCATATAGATAACTATG
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGAGATATTGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCCAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGCAAGGAACCAACTGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGTAATGAGCTCCATTACAGAAAGTGGAAACATAAGAGAACATGAAAGGGCAGA
ATATCAAACAGTAAAAGGGATGATAAGATGTTGAACTGAGTATTGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAGAAACACATTACCATTTGTGAA
TTGTTCTGAACTTAAATGTCACAAAAACAACTTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAAATATTCTAAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSLTLEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFOKTTEFDT
NSTDIALKVFFFDSDYNMKHIHPHMNMGDYIINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTILELEKITFTLSHRKVTDRYRSLCAF
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGSPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVINYKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGA AAAAATAAACATTACATTAAGTCATCGAAAGGTACAGATAAGGTATA
GGAGTCTATGTCATTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTTGCTTGCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCCTCCAGCCAAGAACCTCGGGGCCCTGCGCGGTGGGAGGAGTTCCCCGAAACCGGCCG
CTAACGAGGCCCTCCCTCCCGCAGATCCGAACGCCCTGGGGCTACCCCGGCTGGGA
CAAAGAGCCGCCCTGCTGCCCGGGGGGGAGGGGGCTGGGGCTGGGCCGGAGGCCG
GGTGTGAGTGGGTGTGCGGGGGCGAGGCTTGATGAATCCCATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCGTAAGGCGCTACTATATAAGGCTGCCGCCGGAG
CCGCGGCCCGTCAGAGCAGGCCGCTGCGTCCAGGATCTAGGGCACGACCATCCCAACCC
GGCACTCACAGCCCCCGCAGCGCATCCCGCCGCCAGCCTCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGGGGTGTGTTGACGTATGG
ATCCCTGGCCGGCCTCTGGCTGGCGGGGCCCTCGCCCTCTCGGA CGGGGCC
CCACGTGCACTACGGCTGGGCAGCCCCATCCGCCTCGGGCACCTGTACACCTCGGCC
ACGGGCTCTCCAGCTGCTTCTCGCATCGTGCAGGGCTGGA
CTGAGGACTCGGAGATCAAGGCACTGCGCTCTGCAGGGACCGTGGC
CGTGCACAGCGTGGGTACCTCTGCATGGCGCCGACGGAAAGATG
ACTCGGAGGAAGACTGTGCTTCAGGGAGGAGATCGGCC
TCCGAGAACGCCCTCCCGTCTCGAGCAGTGC
CAGAGGCTTTCTTCACTCTCATTTCTGCCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCATTGGAATCTGACATGTTCTTCGCC
GACCCATTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTT
GAGAAGTAAC
GAGACCATGCCGGCCTCTCACTGCTGCCAGGGCTGGTACTCG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTGTCACATATTCAAGGTTTCCATTGGCAGTGC
CAGTTCTAGCAATAGACTTGCTGAT
CATAACATTGTAAGGCTGTAGCTGCCAGCTGCTGCC
GGTGTGGACAGCTGCTGCACTGCTCAGTTCTGCTGA
TCACTCTTGGAAAATTCTATGTCAGCTGAAATTCT
CC CAGGAGCAGCCAGAAGA CAGGCAGTAGTTTAATT
CAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCTCAACCCCATGTGGAAATT
GATCTATCTCTAATTCCAGGG
ACCATTTGCCCTCCCAAATCTCCAGGCCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCC
CTGAGGCCAGTCTGT
CTGAGGATGCTGCTCTGAGA
TTC
CTCC
CCC
TTG
CCT
CCC
TTG
CCT
CCC
TCT
CTT
TTT
TTT
GTA
TAA
AGG
TTT
GTT
GT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEKAVALRTVAIKGVHVSRYLCMGADGKMQGLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CC CAGAAGTTCAAGGGCCCCGGCCTCGCGCTCCTGCCGCCGGACCTCGACCTCCTCA
GAGCAGCGGCTGCCGCCGGAAAGATGCGAGGAGGAGCGCCACCGCCTCCTGCTG
CTGCTGCCCTACCTGGTGGCTGCCCTGGCTATCATAAGGCCTATGGGTTTCGCCCAA
AGACCAACAAGTAGTCACAGCACTAGAGTACCAAGAGGCTATTAGCCTGCAAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGGAGAAACTGGTCGGAGTGTCTCCTTGCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGCGGGAAATATCGTTGTGAAGTTAGTGGCCCATCTG
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCAGTCAGTCAGTCAGTCAGTCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGATCCAGCTCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAGTGGAACT
CTGCAATTAAACTGTTCCAACCTGGACACTGGAGAATATTCTGTGAAGCCGCAATT
TGGTGGATATCGCAGGTGCTCTGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAATGTGCAGTGGCTCACGCCCTGTAATCCAGCACTTGGAAAGG
CCCGGGCGGGCGGATCACAGGTTCAGGAGTTCTAGACCAGTCTGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGGCTAGTGCAGTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAAAATAGCTTGATATTCA

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKIGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSALS GTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNI SGGIIAAVVVVA
LVISVCGLGV CYAQRKG YFSKETSFQKS NSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTTAAATTTACTCTAAATAA
ATGAATTACTCAATCTCTATGACCACATCATACTACATCACCTTCAAAAGTACATCAATA
TTATATCAATTAGGAAATAGTAACCTCTCTTCTCCAATAGCATGACATTTTGACAATG
CAATTGTCGCACTGGCACTTATTCTCAGTGAAGGAAAACCTTGTGGTTCTATGGCAATTCA
TTTGACAAATGCAAGCATTCTCTTATCAATCAGCTCTTACTAACCTAGCACTGACTG
TGAATCCTTAAGGGCCCATTACATTCTCAGAAGAAAGTAAGATGAAGGACATGCACT
CCGAATTCTATGCTACTTGGCTAGCTATCACTACACTAGTACAGCTGTAGATAAAAAG
TGGATTGTCACGGTTATGTACGTGTAAATCAGGCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACTTCCCAGGCAGATTGCC
AGCTAACACAGACATTCTCTCAGACTAACAAATATTGCAAAATTGAATACTCCACAG
ACTTTCAGTAACCTTACTGGCTGGATTATCTCAAAACAAATTATCTTCAGTCACCAAT
ATTAATGTAAAAAAAGATGCTCAGCTCTTCTGTGTACCTAGAGAAAACAAACTTACTGA
ACTGCTGAAATGTCTGTCGAACGTGAGCAACTTACAAGAAACTCTATATTAACTACAACT
TGTCTTCTACAAATTCACTTGGAGCCTTATTGGCTACATAATCTCTTCGACTTCATCTC
AATTCAAATAGATTGAGATCACAGTAAGTGGTTGATGCTTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCAAATTATCAGAATCAAAGACATGAACATTAAAGCTCTTATCA
ATCTTCGACGCTGGTTAGCTGGTATAAACCTCACAGAAAATACAGATAACGCCCTGGTT
GGACTGAAAATCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTCCTAAAGGTTGTAATCTCAAATTGGATCTAAATAAAATCTATTAAATAGAA
TACGAAAGGGTGGATTTAGCAATATGTCACACTTAAAGAGTTGGGATAATAATATGCCT
GAGCTGATTTCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACACCTAGATTGCTTACATTACCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCAGTGCCTGTACCATGGTACCTGGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATAACAGTAAACCCCATCAGGTGACTGTCATCCGTTG
GATGAAACATGAAACAAAACCAATTCTGATTCTGAGGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCAAGGTCAAGATGTTGGCAAGTGCATTTCAGGGACATGATGAAATTGTT
CTTCCCTCTTATAGCTCTGAGAGCTTCTTCTAATCTAAATGTAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTGAGCAACAGCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAATCTTGCCTAAATACCCCTGACAGACAAGTCTATGTCATTCTGAGGGAAACACTA
GATATAAAATGGCGTAACCTCCAAAAGGGGGTTTATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATTAATAAGAGATATTCAAGGCCATTCACTGGTTGGTGTCTGGAAAGCA
AGTCTAAAATCTCAAATCTAGTGTAAATGGACAGCCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGCAATACCATCTGATGTCAGGTTATATACTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAATGTCACCACCAAGGTTGCAACCTGATCAAAAAGAGTATGAAAAGATAATAC
CACAAACACTTATGCCCTGTCCTGGAGGCCTTCTGGGATTATTGGTGTGATATGCTTATCA
GCTGCCCTCTCCAGAAAATGAAACTGTGATGGTGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGTGATTAGGTGAGCTTATCCTCTGATAAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTACCAACAAATATGCTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTGDLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNSNLQELYINHNLSTISPGAFIGLHNLLRHLNSNRQMINSKWFDAL
LPNLEILMIGENPIIRIKDMNFKPLINLRSVVIAGINLTERPDNALVGLENLESISFYDNRL
IKVPHVALQKVVLNKFLDILNKNPINRIRRGGDFSNMLHLKELGINNMPELISIDSIAVDNLPD
LRKIEATMNPRLSYIHPNNAFFRLPKLESLMLNSNALSAHYGHTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPNSLN
EAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSPQDNNGSLNIKIRDQIANSVLVSWKASSKILKSSVKWTAFV
KTENSAAQSARIPSDVVKVYNLTHLNPNSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQE
YEKNNTTTLMACLGGLLGIIVCILISCLSPEMCDDGHSYVRNYLQKPTFALGELYPP
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTGTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTCCCTCTCCATGTGTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCTAACGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTGAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATGGATTCAAAG
TGTGCAACAAAATGCCITCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCAGATTGCACTAGAAATAAGTGGTTACTTCTCCCATCCATTGAAACATTGAA
ACTTTGATTTCACTGAGTTTTGAATTATGCCACTGCTGAACCTTAAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACCTTGAAACCATGGGAAAAAAAAAAAAAAACAA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMCPCGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFFNNLKRARIANNPWHCDCTLQQVLRSMASNHETAHNVICCKTSVLDEHAGRPF
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGGGACCGAAGGCAGCCTGGAGATGCAAGGTGAGCAAGAGGAATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCTGGCAGCCCACCTCTCTGCTGGTGT
GGGCTCAGTCAGTCAGGCTCGGCCACGGCTGCCGCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTCTTGCTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACCGCGCTGTGACCTAGGCAAGAACCGCATCAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCCCACCTGGAGGAGCTGAGCTAACGAGAACATCGTAGGCCGTGGAGGCCGGCG
CCTTCAACAACACTCTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGGCTCTCACTGGCTCAGCAACCGTACAGCAGGACATCAGCGAGAACAAAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACACACTCAAGTCACTGGAGGTTGCC
ACAATGACCTCGTCTACATCTCACCGGCCCTCAGCGGCCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTTCATCCCCACCGAGGAGCTGCTCCACCTGCAAGGCCCT
CATCGTCTGGGCTCCGGCACCTAACATCAATGCCATCGGCCACTCTCAAGAGGCC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAAC
TGCCTCTACGGCTCAACCTGACGCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCGCTTCTCAACCTCTCTACAAACCCATCA
GCACCATGGGGCTCATGTTGCATGAGCTGCTCCCTGAGGGAGATCCAGCTGGTGGGC
GGGAGCTGGCCGTGGTGGACCCCTATGCCCTCGGCCCTAACACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACGCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCGCTGGCTGCGACTGTCGGCTCTGTGGTGTCTGG
CGCCGCTGGCGCTCAACTTCAACCGGAGCCAGCAGGCCACGCGCCACGCCAGGTTGTCCA
GGGCAAGGAGTTCAAGGACTCCCTGTGATGTGCTACTGCCAACTACTTCACCTGCCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGCGAGGGGCCACACGGTGCAGTT
GTGTGCCGGGCCGATGGCGACCCGCCGCCATCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCTGTATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGAAACCGCACGTACCTGTGCATCGGCCAACGCCGGGCCACGAC
TCCATGCCGCCACCTGCGATGTGCGAGCTACTCGCCCGACTGGCCCCATCAGCCCAAACAA
GACCTTCGCTTTCATCTCAACAGCGGGGAGGGAGGGGCCAACAGCACCCGCCACTG
TGCTTCCCTTCGACATCAAGACCTCATCATCGCCACCAACATGGCTTCTACTCTTTC
CTGGCGTGTCTCTCTGCTGGTGTGCTGTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTCGGGGAAAGTCGGACGCAGGATCAGCTCCGCCG
ACGCCGCCGCAAGGTTCAACATGAAGATGATATTGAGGGCGGGGGGGGGGGGAGGGGACCCCCG
GGCGGCCGGGAGGGGAGGGGCTGGTCGCCACCTGCTACTCTCCAGTCTTCCACCTC
CTCCCTACCTTCTACACAGCTCTCTTCTCCCTCCGCCCTCCGTCCCCCTGCTGCCCG
CCAGCCCTACCCACCTGCCCTCTTCTACAGGACCTCAGAAGCCAGACCTGGGACCCA
CCTACACAGGGGATGACAGACTGGAGTTGAAAGCCAGAACCGACGCCAGAGTC
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGGTTCAATAATTATGGATTT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCESAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNIKTLNQDEFASFPHLEELNENIVSAVEPGAFNLFNRLTL
GLRSNRKLIPPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLSQLTLEKCNLTSIPTEALSHLHGLIVLRLHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSISITHCNLTAVPYLAVRHLVYLRFLNLNSYNPISTIEGSMILHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTLEESVFHSVGNLETILIDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKNSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSQDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCGCACCTCGGCCCCGGGCTCCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCATCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCGGGAAAGCGCGATGGGGGCCAGCCGCTCGCTCTGCTCTGCTCTGC
TGTTCGCCTGCTGCTGGCGCCCGGGCAACCTCTCCCAGGACAGCACGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTGTCAAGTGCCAAGTGAAGATCA
CGAGGACTCATCCCTGCAATGGTCAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTACACCTGCTCAGCAGACTCTACTTGGGAGAAGA
ATCAGCAATGTGGCCCTGGCAGACGAGGGCAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAAGTGCCAAGTCCCTGTCAGTGTCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTCATTAACGGGAAAAAGACACGCCACCCCTAAACTGTCACTGCAGTCAGTCTTCTGGGAGCAAAG
CCTGCAGCCCCGCTCACCTGGAGAAGGGTACCAAGAACCTCACGGAGAACCAACCCGCAT
ACAGGAAGATCCAATGGTAAACCTCACTGTCACTGCAGCAGCTCGGTGACATTCAAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGGAGGGCAGAACAGCTGTGTACACTGTGAGGGTCGGCAATCCAGTCC
CCCAAGCAGTACCTATGGGAGAACGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGT
GCCCTGATCTCCCTTCTCAACAAGAGTACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGCAGCTACAAGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCACTACTTGATCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACCGATGCTCCAGCGGACACGGCATCATCAATGCGAGAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATTCAAGGGCGCTGCCACTTCTGC
GCCCCCAAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTGGGGTGCGBTTTGTACTCGTTGGAAATGGGGAGGGAGGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCAATTGGTTATTATTATTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLCQVKDHEDSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCCCACACCGCTTCTCTCTTTCTGG
CTCGGACATTGGAGCACTAAATGAACITGAATTGTGTCGCTGCTTAAAGCAGGATGGCCTG
TTACTTTGTGATGAGATGGGAGTAATTGCTCGCTTAAAGCAGGATGGCCTG
GCTGGAGACGCTCTTTGCGCTGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAGGGCTTCACA
AGTCTGAGCGCTTCACTGCCCGACTTCCAGTTTACCATTTATTCGATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTAAATGCGGTTAGTTGCACATGG
AAAACAATGCTTGCAATGAGTCGCTGGGGGCTTCTGGGCTGCAGCTGGTGAAG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTCTGGGCTGGACGA
TCTGGAATATCTCAGGCTGATTTAATTACAGAGATAGACCCGGGGCTTCAGG
ACTTGAAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTCGCTCATCACCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGAAATCCTGGTATTGCGAGATCCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATGCTCTCCCTGAAAGAATGGCTGAAAACATTCCAAGATGCC
CTGATCGCCGAGTGGTCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC
CCCGAACAGGACTTGTGCTTGGAAACAGGACTTGTGCTCCGGCCCTGCAAAC
GGGAAAGAGAACCTTGTGCTCTGGGACCCCTGCAAACCTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGCTGCTGCTAACAGGGAGTAAAGAATCCCAGGCAACTGGCAGAT
AAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCCGGGCTGAGCTGCGACCACATCCAGGGTGGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTTGGCTGATTTGAAAGCCAAAGCTCTAACGTCAGGA
GCTTTCTCAGAGATAACAAAGATCCACAGCATCCGAAATCGCAGTGGATTACAAGA
ACCTCATTCTGGATCTGGCAACATAACATCGTAGTGTAGAGAACAAACATTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTCTGGG
GAAATTCGCGGGGCTGCAAACCTAGAGTACCTGAACGTTGAGTACAACGCTATCCAGCTCA
TCCCTCCGGGCACTTCAATGCCAACACTGAGGATCTCATTCTAACACAAACCTG
CTGAGGCTCTGGCTGTGGAGCTTGCCTGGGGCTCGCTCTAAACTCAGCCTGCAACAA
CAATTACTCATGTAACCTCCGGTGGCAGGGTCTGGACAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGCCTCTGCACAATTGTCCTTCAAGCAGTGGG
GAACGCTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCGGTGAACCTCTT
TAGAAAGGATTCTCATGCTCTCTCCAAATGACGAGATTCGCCCCAGCTGTACGCTAGGATCT
CGCCCAAGCTTAATTCGACAGTAAACAGCAGCTGGGTTGGCGGAGACGGGAGCGCAGCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCGGTGTTGGTCCGGACTGCTGCTGGT
GTTGTCACTTCCGCCCTCACCGTGGTGGCATGCTGTTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACCTCCGGCTCGAGATTAAATCCCTACAGACAGTCTGT
GACTCTTCTACTGGCAAAATGGGCCCTAACAGCAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAGACCCCAACCTCAAGGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCGCG
CCATCAGCCTGATGGCATAAGTAGATAAAACTGTGAGCTGCACAAACCGAAAGGGCCT
GACCCCTTAATTAGCTCCCTCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGCCAGCACGACCCCTGCTGGAAAG
AACTGACAGTGGCCCTCGGCCCTCGGCCCTGGGGGGCTGGGGTTGGATGCCGCGGTTCTATAC
ATATATAACATATATCCACATCTATAGAGAGATAGATATCTATTCTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGATGAATGTAT
TGTAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVITGVCCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTA
LFLHGNSLTRLFPNEFANFYNAVSLHMMENGLHEIVPGAFQLQLVKRLHINNNNIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLIILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPIGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSLAPPQAQETTFAPGPLPTPKTNQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHIPGSGLKMMNCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKMLILLLDGNNNNIATVENNTFKNLLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNALIQLILPGTFNAMPKLRLILILNNNLLRSLPVDFAGVSL
SKLSLHNNYFMYLPVAGVLDDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFRRKDFMLLSDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLTVFTSAFTVVGMLVFLRNRKRSKRNDARSSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCCGGCGCAGCTGTGTTCTGACCCCAGAAATAACTCAGGGC
TGACCGGGCTGGCAGCGTCCGCACACATTCTCTGCGGGCTAAGGGAAACTGTGGC
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGTCGTGGAGCGAGGGGGGGGG
AAGGGAGGGGGAAACGGGTTGGGAAGCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCAAGTTGGAGCAGCTCTGCGTGCAGGGGCTCAG
AGAATGAGGCGGCGTGGCTCTGTGCTCTCTGCGAGCGCTCTGGCCCGGGCGG
CGCGAACACCCCCACTGCCGACCGTGTGGCTGCTGCCCTCGGGGCTGCTACAGCCCTGC
ACCACGCTACCATGAAGCGGCAGGGCGCAGAGGGCGCTGACATCTCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGCGCGAGCTGCCGCTGTGCTCGCGCTCTCGCGCAGGGCCAGG
GCCCGAGGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGGCAGGGTTCCACT
GCACCCCTGGAGAACAGGCTTTGGGGTTCTCTGGCTGTCTCCGACCCGGGCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTGCAACCGCGCGAGATGCGC
GGTACTCCAGGGCACCGGTGGGTCGAGCCCGCAGCTGGAGAGATGCGATGCCACCTGC
GCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCTGCGCCGGGGGG
GCCGCTCTAACTTGAGCTACGCCGCCCTCCAGCTGCACAGGCCGCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGGGGGACAGCTCCGATCTCAGTTACTTGCA
TCGGGAGCAAAATCGCGCTCGCTGGGACAACATCTGGGCGATGTGTTGTGCTCTGCC
GGGAGGTACCTCCGTGCTGCAAATGCGCAGAGCTCCAACTGCCTAGACGACTTGGGAGG
CTTGCTGCGAATGTGCTACGGGCTTCAGGCTGGGAAGGACGGCGCTTGTGATGACCA
GTGGGGAGGACAGCGACCTTGGGGGACGGGGTGCCACCAGGCGCCCGGGCCACT
GCAACCAGCCCCGTGCCGAGAACATGGGCAATCAGGTCGAGAGAAGCTGGGAGAGAC
ACCATTTGCTCTGAACAAGAACATTCAAGTAACTCTGGGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGCTCCCTCAAGCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTATTCCAAGTTAACTCACGACTCCCTGCACTCCTCAGGTTT
CGACTCCTCTGCGCTGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGGTGTACT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAAAGCCCTCTTCCCAGCCA
AGGAAGGAGTCTATGGGCCCCGGGCTGGAGAGTGTACTCTGAGGGCTGCTTGGGCTC
CAGTTCTGCACATTGACAAACAATGGGGTAAAGTGGGGACTGTGATCTGGGAGAGAG
CAGAGGGTGCCTTGTGGCGAGTCCCTTGGCTCTAGTGTGCA**TAGGAAACAGGGAA**
CATGGGCACTCTGTGAAACAGTTTCACTTTTGTGAGAACAGGGAAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGAGAAATCCCCCTTCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACACTGCACACTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTGGGGACGGGGTAGTGTGGGGAGAGATATTCTTATGTTATTGGAGAA
TTGGGAGAAGTGATTGAACTTTCAAGACATTGAAACAAATAGAACACAAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAGGAAATGTCTATGTTCTAGGCTAGGAGTAT
ATTGGGTCGAATCCCAGGGAAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRAFAFLCLLWQALWPONGGGEHPTADRAGCSASGACYSLLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGSKDLLFWVALERRSHCTLENEPRLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCSTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPCTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLРАГKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRPPATA
TSPVPQRSTWPIRVDEKLGETPLVPEQDNNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSAAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPPEAALGSSSAHCTNNGVKVGDCLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGGCTGGGATTCAAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCCTTAAAAGTCCTCCGCCCTGCCGGCGCTATC
CCCCGGCTACCTGGGCCGCCGCGGGCGTGCAGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGCGGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGCCCAGCGCGCCGGTGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGCAACGCGCTGGGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTGTTCACTGTGGTGGCATCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGACTGTACCCCTCAATAGCAATGTAATTGGAAAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTCCGATTATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTACAATGGCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCACTTGGGCCCTGGAGCCCTTGTGCTGCTGGCAACAAGATGATGCTGCA
TGATTTCGTGATGCCAACACAGCTGGCAATGGCTTATGCCATGTTCTCGCTGCTGAACCA
AACGAAAGAGGGGATCACTATTGTGGAGGACTCTTCAAGACACCTCCGGCTTTAAAAC
CCCCAAGTGGCCAGACCGGATTACCTGCAGGAGTCACTTGTGTGGCACATTGTAGGCC
CAAAGAACATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCACAGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCCATTGTGTCAGAGAGAAATGAATTCTTATTCA
TTTATCAGACTTAAGTTAACAGCAGATGGGTTATTGTGTCAGTACATATTCA
AAACTGCCTACAACTACAGAACAGCCTGTCACCACACATTCCCTGTAACCAAGGGTTAAA
ACCCACCGTGGCCCTTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAGTGAATTGTGATTAGCAGCTGTTATCACAAACATCTCGCGATGGAGTTG
CACGCCAACAGTCTCGATCATCAACATCTCAAAGAGGGGAAATTGGCGATTCA
CAAGAACATGAGTGCAGGCTGACTGTGCTCTGCAAGCAGTGCCTCTCCAGAAGAGGTC
TAAATTACATTATTGGCCAAGTAGGTGAAGATGGCGAGGAAATCATGCCAACAGC
TTTATCATGATGTTAAGACCAAGAACAGAAGCTCTGGATGCCCTAAAAATAAGCAATG
TTCAGTGAACTGTGTCATTAAAGCTGTTATCTGCCATTGCCCTTGAAGAGATCTATGTT
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAGTTCTT
TGCTGCTGTCAAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTGTGGTGTAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAGCGTTATTATACATCTGTAAAAGGAT
ATTAGAATTGAGTTGTGAGAGATGTCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
GTTATTGTTCAACCTTCAAGCCTTGCCTGAGGTGTTACAATCTTGTCTTGGCTTTCTA
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNCRYDYVAVFNGGEVNDAARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSSLTADGFIGHYIIFRPKKLPTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGEDGRGKIMPNSFIMMFTKNQKL DALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACCGTGGCGGCCACGGCGCCGCGGCTGGGCGGTGCGCTTCTT
CCTCTCGTGCCTACGAGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCCACCTCCCCAGTCTCTCCCCGCCTCAGCCCCATCCGTGTCATAACCTG
CCGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTGTCAAATAACAAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGCAAGCAAGTCAGACTTCAGTGCACCGCCTGCTGGAGCT
GAGTGGAGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGTACGGCAGTGTGAAGGAGAAGG
GACACGGGGGCAGGGCACTGTGACTGCCAAGCCGCTACGGGGTGAGGCCGTGGCC
AGTGTGGCCTGGTACTTGAGGCAGAACGCAACGCCAGGCATCTGGTATGTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACACTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGCCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCATGAGTGTGCCAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGAGAGA
ACAAGCAGTGTAAAACCCGAGGGCGGTTATGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATGTGTGAAGGAGCAGATCCCAGTGTGAGCAGGCTTCTTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTGGTGTTCACGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTGAGGCCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCCTCCACCCACCGCTGCCAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGGACTGGCAGGCTCACAATGTGTG
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGGCCATCACAGCTCCCTCTGCCAGCTGCTGCACTGCTGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATGCCACTTATTATTCACTCAGGAAATAAGA
AAGTCTTGGAAAGTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGGLVPAVLWGLSLFLNLPGPIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVC SKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLCPCGGTERPCGGYGC EGE GTRGGSGHCDCQAG
YGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGGSYE CRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFSEMTEDELVVLQQMFFG
IIICALATLAAGDLDLVFTAIFIGAVAAMTGYWLRSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTTGTCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCAGCCCCGG
GCCGCCCTGACCGGGGAGCAGCTCTGGGAGCAGCTGCTGCCAGCTGAGCTAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTGGAGGCCAGCACACACCTGCTGGTGGTC
CATGGAGCAGCGCTGCCGCCAACAGCAGCTGGTCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAACAGGCCGCGCTGCACAGGCACGGGCGCTGCTCCCGCGCAGGCCCGGGC
CGGGTGACCGTCAGTGCGCTGCCGACGACGGCTCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTACAGGAGGCCGCTGGAAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGAGCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCGCTGGCGTCCGGGCCACAAGCTGGTCCGCTTGCTCGCAGGGCC
GCCAGCCGGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCTTCAAGTGGC
CGTTCTGGGCCCTGACAGTCGCTGCCGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCGACTGTGCCCTCGGATGGTGCCTGGCCAAGGAGGCTCCAGCCATAGGCGCTAGTG
TAGCCATCGAGGGACTTGAATTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG
GCGATGACTGAATGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTTCTCAGGAATGAGAAATCTTGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCTGTAC
TGGATCTGGCTAAAGTCCTCCACCACACTCTGGACCTAAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCATCCAGATAATAAGACTTTGTAAAACATGAATAAAACACATTATTCT
AAAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFSREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCCGCTGTTGTCAGTGGCCTGATCGCAATGGGACAAA
GGCGAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTCCTACTCGGCTTTCTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCAAGACTCGTTGCTATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAACCTGATCACCTCAAGTCGTACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCCTCATCCAAGCCTACAGTTAACATCCCCCTCTGCCACCATTGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGTAGGCCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAAGGAGAGCTGGCTTTGATCCCTGTCAGCCTCTGATACTGGAGAACATA
GCTGTAGGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCTGGGAAT
CTTGGTTTTGGCATTGGTTGCCTATAGCCGAGGCCACTTGTACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTCCCAGAATGTAAGGAGAACATCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGATTGCTTACT
CAGGTGCTACGGACTCTGGCCCTGATGTCGTAGTTCACAGGATGCCATTGGTCTTACT
TACACCCACAGGGCCCCCTACTTCTGGATGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTCTACCCTGAGTGGCTGGAACTTGTAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGAAAAATGGGGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTGAGCTGGCTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGGTGG
TGATGACACTGGGTCTTCATCTCTGGGCCACTCTCTGTCCTCCATGGGAAGTG
CCACTGGGATCCCTGCGCTCTGTCATCTGCAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGGCTGGGATCAGCCTGACCA
ACATGGAGAAACCCACTGGAAATACAAAGTTAGCCAGGCTAGGGTGCATGCCCTGAGTC
CCAGCTGCTCAGGAGGCCTGGCAACAGAGAAAATCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGVIMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNFGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GGCGTGGCGAACAGGGGCTCTGGGCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGAGCCCGTTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCACCACCAAGTTCCAGTGGCAGCGATGGCAGCGATGAGGAGGTGCAGGATTGAGCC
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCTCCCTGCCCTGCACGGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCAGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG
GGGATGCCACACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGAAGGCCAACTGCCATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGAAGCCTGGTCACCGCACCCCTCCCTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGTGGAGGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCACGTGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGGTNEILPEGDATTMGPVVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSPL

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACACGCGTCGGTCTCGCTCGCTCGCAGCGGCCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGGGGGAGGGCGAGGAGGAAGGAGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGGATGAAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCGTGGTTAGCTGGCGTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTCAAGTGTGTGCTGACCCGGCATTCCGAGAATGGCTCAGGACCCCCAGCG
GAGGGGTTCTTGAGGCTCTGTAGCCGATTTACTGCCAACGAGGATTCAAGACTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGAAACCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCAAATGAAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATCAAGATCCGG
TACCCCGACCTACACAAATGGTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGTTACAAAACCTTATCTGGTGTCCAGCCCACCCCGGTG
CTTGCTCTGGAAGCCAAGTCTGCACTACCTCAAATGGTAGTACGGAGATTCTGCT
GCCACCCGCGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAAGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGAACCAAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTTCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGAGTGACCTGACTTGTGGTAGACGGCGTGCCTAGGCCCCGGTACATGGCCTCTGGGGCCAG
ACGAAGCTGTGAGTGCGGCTTGAGTGCTTAGGCCCCGGTACATGGCCTCTGGGGCCAG
GGCTGCCCTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTCTGAGCTGCTCCAA
GTCTGTATTCACCTCCAGGTGCAAGAGAGCACCCACCCCTGCTCGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGGAGGTGGCATCCACCAAGGCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTGCTGAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCCCTCTGGTTTAGACAAATGTAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLVDDQSPPAYPGSGD'TD'TGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCGGCCCTCCCCCCCCTCGCTCCGTGCGGTCCGTCGGTGGCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCCTGCCCCCAGCCGCTCACCG
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGGATGAGGCCGGAACCCGCTACAGG
CCGTGCTGCTGGCGTGTGCTGGTGGGCTGCGGGCGACGGGTGCGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCCTGTTA
TAAAGTCATTACTTCATGATACTTCAGAAGACTGAACACTTGTAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACATTCAATTGCAAATATTCTGATGAGAACAGCAGTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCTGAAATCTGGCTACAT
CTTAATCCCCAGCATTCCCTTCTCCTCTGTGGTACCAACAGTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGGAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AACGCAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAAATTTCATTCCAGTGTGTT
CCGGAGAAGCCACTCCGATGACATGCTTGTGACTATGACAACATGGCTGTGAAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTACGGTACGGTGGAGGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGCTGGATGGTGGAAATGAAATATG
GTTATTAGGACATATAAAAACGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGCTCTGT
GGATGAGCATGTTGCCCCACGACCTCTGTTGGACCCCACTGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCATTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTTGGAAAACCACCTCTGTTCCCTTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCACATATGGTAGCACAG
GTTGGCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

M R P G T A L Q A V L L A V L L V G L R A A T G R L L S A S D L D L R G G Q P V C R G G T Q R P C Y K V I Y F H D T S R R L
N F E E A K E A C R R D G G Q L V S I E S E D E Q K L I E K F I E N L L P S D G D F W I G L R R R E E K Q S N S T A C Q D L
Y A W T D G S I S Q F R N W Y V D E P S C G S E V C V V M Y H Q P S A P A G I G G P Y M F Q W N D D R C N M K N N F I C K Y
S D E K P A V P S R E A E G E E T E L T T P V L P E E T Q E E D A K K T F K E S R E A A L N L A Y I L I P S I P L L L L V
V T T V V C W V V I C R K R K R E Q P D P S T K K Q H T I W P S P H Q G N S P D L E V Y N V I R K Q S E A D L A E T R P D L
K N I S F R V C S G E A T P D D M S C D Y D N M A V N P S E S G F V T L V S V E S G F V T N D I Y E F S P D Q M G R S K E S
G W V E N E I Y G Y

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCGCAGAAGACTTG
GTTTGCCCTCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTTCAAGCATGCGTTGTGGACCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTCAGGTCTGTTTGACACGGGGCTCGGAGTCCCTCAAGCC
GCTCCCCTGAGGAGCAGGTAGAGTGGAAACCCAGCTATTAGAGGTCCCACCCCAAACCT
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTTATTGCTTCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAGGCCATCATCAT
CCACACTGATGAAGCAGATTCAAGAGTCTGTATCCAACCTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACAGAGGCCGGAGGAGACTGCCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTCAGATGGCAGTAGGCCATTCCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCCGCTCATGATG
TGACCTTCATACCGCTTAATGACCCGGGATTGACCAACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEQVEWPQLLEVPPQTQFDYTVTNLAGGPKPYSYDSQYHETTLKGGMFAGQL
TKVMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRTASLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPSCPMLKRFAWMIEQRADVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYYAAHDVTIFPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACATAATTTGCTGCTGGGGACCTCCTTAGCCT
TAAATTTCAGCTCATCACCTTCACCTGCCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGACCAGACCTGGATTCTCTAGCGTCTCCATCTGGAGTGCCTGGCTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGAACAGAAAGGCCAGTGGGACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTGCCCCAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGGCCACCAGCAGAAAAAGAGCAAAGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGCATTGCAAGGGACGCTGGAAAGTGA
GCACCAAGAACAGTGGTATACCGTGTGCCAGACAGGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGAGCTGGATGTGGAGGGTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAACGAAACCCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCAGATGTAAGAACACAGTGGGTGG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGGCCGCATCTGGCTGGATAATGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGGTTTCAGCACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAACAGAAGGGAGCATTTACTGCTACATGACTGCATGGGATGAAACACTGATCT
TCTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCATGTCACACAGCAGATTCCCAGCCTCCATAATTGTTGAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACATA
CACCATTGCTCTGTTCTGAAGAACCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAAATAAAAGATAGCAC
TATGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVCSTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVHLKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGGGACCGCGTGGCGGACCGTGCGGGCGCTACCAGGAAGAGTCGCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG
CGTCTTCGGCTCTTCCGGCTGCTGCAGTGGTGCGCGGAAGGCCAACCTGCGGAATGCTG
TGGTGGTGATCACAGGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGTCAAACCTGGTGCTCTGTGGCGGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGAC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACATTGTCACAACATGCTGGGATCAGTACCGTGTACCATCATGGACACCACAGTGG
TGTGGACAAGAGGGTCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCAGGGCAAG
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCAGGGCAAG
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCACCCAGGTTCTTGAA
CTGTCTGCGTGCAGAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGGGATGGATCTAGGTATGGATTATGGAC
ACCACCCACAGGCCAGGGCGAAGCCCTGAGGTGGCCAGGATGTTCTGCTGCTGTTG
GAAGAAGAAGAAGATGTGATCCTGGCTGACTTACTGCCTTCAGGGCAGAAAAGAGCGGAAATCC
CTCTGGCTCCTGGCTCTTCTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGGAAATCC
AAAGAACTCCTAGTACTCTGACCGCCAGGGCCAGGGCAGAGAAGCAGCACTCTAGGCTTG
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTCACAAGTGG
AAAGACTGAAGAAAACACATCTGTGCAGATCTGCTGCCAGAGGACAATAAAAACGACAACA
AGCTTCTCCAGGGTGAGGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAAACTAGAAAATAAACATCTAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGAGAGCTGGCCGCATGGCCAACTTGTATTGAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGLVQFRLLQWVRGKAYLRNAVVTGATSGLGKEAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPVLTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTVVDVKRVMETNYFGPVALTKALLPSMIKKRQGHIVAISSIQGKMSI
PFRSAYAAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVVAQDVLA AVGKKKDVLADLLSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLLPPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKGLGAKVHTVVDCSNREDIYSSAKVKAEIGDVSLVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDLAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCGGCGGACCGCGTGGGTCGACTAGTTCTAGATCGCAGCGGCCGCGGCTC
AGGGAGGAGCACCGACTCGCCGCACCCCTGAGAGATGGTTGGTGCCTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCACCCCTAACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAAATTGAGTTGGTGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATACAGGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGAAACATGGCCCTATGGTCACAAGTAACATGA
CCTTGGCTGACAGAGACTCCCTGGACACAAACGCTCCATGTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACTAATCAGTTTITCCAGATATTCCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTCAGCCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACCGAATTGCTATTGG
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTCCAGAAGCAGTGCCATGAATGCATAAACACATC
AGGAAGCAGAACTGGTTGAGGCCCTTGAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAGTGCATCCTCTTACCTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGCGGT
GACCGGAACCTGAGGATCAGCTTACTATGTAATTGGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTTGAAAAGTACTTGCAGA
AGATAACAGTACAGTCAGTTAACGCCATGTTAATGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGCCAATGCCATCATGTCAGTGCCCTGACAGAGCGCTCTTGATGGGC
ATGGACTGGAAAGGATCCAGGAATACAAGAAGGCCAAAAAAAGTTGGAAAGATCTTAA
ATCTGACAGTGAAGTGGCTGTTACATCCGGCAAGCGGGTGACTTCCATCAGGAATTATT
GAGGTGGAGGACATATTACCCATGACCAGCCTCTGAGAGCTTGTACATGATTAAATCGA
TTCATTTATGAAAAGGATGGATCCTTATGTTGGAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCTCATCAATAAAAATATCCTGAAACAAAGTGC
TTTGTTTGGGGAGATGTTACTACAAAATACATGAGTACATGAGTAAGAATTACA
TTATTAACCTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAGATGTATAATGA
AATTTAGGGCTTGAAATAGGAAGTTTAATTCTTAAGAGTAAGTGAAGGTGAGCTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTGGATAAGAATAGCTCAATTATCCCAAATAATGGATGAAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAAGTCTTGAACAAAAGAATTCTTGAATA
AAAATATTATATAAAAGAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGRELSSL
VGFPFPGLNMKSYAGFLTVNKTYNSNLFWFFFPAQIQPEDAPVVWLQGGPGGSSMFGLFVEH
GPYVVTTSNMLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKKYFQKQCHECIEHIRKQNWEAFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWL
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVKWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCGGAATGGCACATGTGGAAATCCAGTCTTGTGCTACAAACAT
TTTCCCTTCCTAACAGTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAAGGGCTGGGGCAGGGCAGGGCAGCTCACTCAGGGTGACCAGCTCTT
CCTCTCTGTGATAACAGAGCATGAGAAAAGTGAAGAGATGCAGCGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCCTAACAGCTTCAAAAAACAGGAGCAGTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAGACTGGGTTAGTCTTAATATCAAATTGACTGGCTGGG
TGAACTTCAACAGCCTTAACTCTCTGGGAGATAGGGAAAAGATGGCTTAAGGGCCAGAAA
TAGAGATGTTGTAATAAATTTAAAAAGCAAGTATTTTATAGCATAAAAGCTAGA
GACAAAATAGATAACAGGATTCCCTAACATTCTAACAGGGAGAAAAGTATGTTAAAATA
GAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAACGGGATGGGACCCCTGGGTC
AGGCCAGCCTCTTGTCTCTCGGAAATTATTTGGTCTGACCACTCTGCCCTGTGTTTT
GCAGAATCATGTGAGGCCAACCGGGGAGGTGGAGCAGATGAGCACACACAGGAGCGTCT
CCTCACCGCCGCCCTCTCATGGAGAACAGGAGCAGCCCTGCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCAGTGGCTGGGCTGCTGGCCCCCAGCAGCCGGC
ATGCTCAGTCAGCACCTTCACTCTGAGAATCGTACTGGACCTCAACCACCTGACCGT
CCACCAAGGGACGGGGGGCGTCTATGGGGGCACTCAACCGGGCTATAAGGTGACAGGCA
ACCTGACCATCCAGGTGGTCATAAGACAGGGCAGAAGAGGACAACAAGTCTGTTACCCG
CCCTCATGTGCAAGGCCCTCAGCGAAGTGTCTCACCTCACCAACATGTAACAAGCTGCT
CATCATTGACTACTCTGAGAACGGCCTGCTGGCCTGTGGGAGCCTTACACGGGGTCTGCA
AGCTGCTGCCGCTGGATGACCTCTTCATCTGTGGAGGCCATCCCACAAGAAGGAGCACTAC
CTGTCAGTGTCAAAAGACGGGCCACCATGTACGGGTGATTGTGCGCTCTGAGGGGTGAGGA
TGGCAAGGCTCTTACGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAAGCTGCCCGAGACCTGAGTCTCAGCCATGCTGACTATGACTACACAGCGAT
TTGTCTCCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGTACAT
CTTCTCATCTACGGCTTGTACTGGGGCTTGTCTACTTCTCACTGTCTGCCAGCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCACTGTGCGG
CTCTGCAAGGATGACCCCAAGTTCACACTCATGTGCTCTGCCCTCGGCTGCAACCGGGC
CGGGGTGGAATACGGCCTCTGCAGGCTGTTACCTGGCAAGCTGGGACTCACTGGCCC
AGGCCCTCAATATCACCGACCCAGGACGATGACTCTTGCATCTTCCAAAGGGCAGAAG
CACTACCCGCCCCGATGACTCTGCCCTGTGCTCCCTATCCGGGCATCAACTT
GCAGATCAAGGAGGCCCTGCAGTCTGTGCTTACAGGGCAGGGCAACTTGTGAGCTCAACTGGC
TGCTGGGAAGGACGTCAGTGCACGAAGGCCCTGCCCCATCGATGATAACTTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
CAGCAGGGACCCGATGCCCTGTGCTCCCTACGTTACAACGGCTACAGCGTGGTTTTTG
TGGGACTAAGAGTGGCAAGGTGAAAAGGTAAGAGTCTATGAGTTCAAGATGCTCAATGCC
ATTCACTCTCTCATGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGAGGTAAAGAGGGGTTAATTTTG
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGTGTGTAAGGAATGCAAGCGTA
TTCAATATTCCTAAACTTAAAGAAAAACTTAAAGGATCAGTGTGAAAGGCTACATCTGCAAAAGCAAA

FIGURE 62

MGTTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVSVLLSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKL TGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAFCPIRAINLQIKERLQSCYQGEGN
LELNWLKGDKVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTCGGACTGGGAGTGGGAACCCGGGCCCCCGCCTTAGAGAACACCGCATGCCA
CGTGGAGGCCTCCGGGGAGGCCCGCACGCTGGACTCTCTGCTGCTGGCTTGGGCTTCTGGCTCC
GCAGGCTGGACTGGAGCACCCCTGGCTCTGCGGCTCGGCATCGACAGCTGGGCTCAGGGCAAGGGCTGGA
ACTCTCATGCTGGAGGATTCCACCTCTGATCTCGGGGCTCACCTCACTATTCCGTGCCCAGGGAGTACT
GGAGGGACCCCTGCTGAAGATAAGGGCTGTGAAACACCCCTCACCCATATGTCGTTGAAACCTGCA
AGCCAGAAAAGGCAAATTGACTCTCTGGAACCTGGACCTGGAGGGCTTCTCCCTGATGCCAGAGATCG
GGCTGTGGGTGATTCTGGCTCCAGGGCTACATCTGCACTGGGCTTACGGAGCTGGACCTTGGGCTAC
TCCAAGACCCCTGGCATGGGCTGAGGACAACCTACAAGGGCTTACGGGACTTACATGTCGTTGCA
TGATGTCAGGGTGGTGCACACTCCAGTACAAGCTGGGGACTTACATGTCGTTGCA
GTTCCTATAATAAAAGACCCGATACATGCCCTAAGGCAAGGCAACTGGGACCGTGCATGTC
TCCTGACTCTGAGAACACAAAGGATGGCTGCAAGGGCATGTCAGGGACTTCTGGCAACATCAACTTGCAGT
CAACACACAGCTCAGCTACTGACCACCTTCTTCAACCTCCAGGGACTCAGCCAAAGATGGTATGGAGT
ACTGGACGGGGTGGTTGACTCTGGGAGGGCTTACAAATATCTTGTGATCTCTGAGGTTTGGAAACCGTGT
CTGGCATTGTGGAGCCGGCTTCCATCAACCTTACATGTCGTTTACGGGAGGACCAACTTGGCTTCATGAATG
GAGCCATGCACTCCATGACTACAAGTCAAGTCACTGGGACTTACATGTCGTTGCA
ATTACAGGCCAAGTACATGAAGCTTCCGAGACTTCTGGCTCATCTCAGGCACTCCCTCTCCCCCACCTG
ACCTCTTCCAAAGATGGCTATGAGCCATTAAAGCAGCTTGGGAGACTTCTGGGAGGACTTACATGTC
TGGGGAGGCAAATCAAGTCTGAAAGGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCT
TCGGGTACATTCTTATGAGACAGCATCCTCTGCTGGCATCTCTGAGGCACTGGGGAGGTT
TGTTGTGAAACAACTGATTCATGGGATCTCTGCTGAGGACTACAAGAACAGAAGATTGCTGTC
ACACCGTGTGAGGATCTGGTGGAGATCTGGGAGGACTTACATGGGGAGAATATTGATGACCAAGC
GCTTAATTGGAAATCTCTATCTGAAATGTCACCCCTGGAAAACCTTCAGAATCTATACCTGGGATATGAAGA
GCTCTTTCAGAGGTTGGCCCTGGGAAATCTGGGTTCTCCCGAAAACCCACCATTAACCTCTTCTTCTTG
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAAGCTGGAGGGCTGGAGAACGGGTTGATTC
TCAATGGCCAGAACCTTGGACCTACTGGAAACCTGGACAGAACCTTACCTCCAGTGGCTTGA
GCACGGGAAATCAACCCAGGTCTGGTTTGGAGGAGACGATGCCGGCCCTGCAATTACAGTTACGGAAACCCCC
ACCTGGGAGGAAACAGTACATTAAGTGAAGGGTGGCACCCCTCTGCTGGGCCAGTGGGAGACTGCCCTC
CTCTGAGGACTGGCTGGTGTGTCAGCTCAAAACCTAACGCTCAGGGAAAGGTGGGATGGCTCTGGG
ACTGGGGGCTCAGTCTGGCTGGCTCTGCTGAGCTCAACCTAACGCTCAGGGAAAGGTGGGATGGCTCTGGG
TGCTTGTGATGATGGCTTCTACAGGCCCTGCTTGTGCGGAGGCTGTGGGCTGCTCTAGGGTGGAGC
AGCTAATCAGATGCCAGGCCCTTGGCCCTCAGAAAAAAAGTGTGAAACCTGGCCCTGACCCGAGTCACAGCC
TGGGAGCATCTGCTGGACTCAGGGTGTCTTGTGCTGGCTCTGGAGGCTTGGGCCACATCCCTCATGGCC
TTTATCCCCAAATCTCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCACCTGAGCTGACTTTG
CTTCTCTCAACACCTCTGAGCTTCTGGGATTCTGGAGGAAACTCGGCCGTGAGAAACATGTGACTTCCC
TCCCTTCCCACTGGCTCTTCCCAAGGGTGAACAGGCTGGGAGAAACAGAAATCTTACCTCTGGCTTCTC
CAAGTTAGCAGGGTGTCTCTGGTGTCTGAGTGGAGGAGCATGTGACTCTGGCAGAACGCCATGGCC
CATCCAGGGAGGAGGAGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCC
AGGGAGGAGGAGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCC
GGAGGAGAGAACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCC
ACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCC
GAAGTGTGTCAGTCAGGGCCCTGGCTTGTGCTGGGGCCAGGCCAACACTGGCTTGGCTACTGTCTG
GTTCAGTAAAGCTATAACCTGAAATCAA

FIGURE 64

MTTWSLRRR PART LGLLL VVLGFLV LRR LDWSTLVPLRLRH RQL GLQAK GWN FM LED STFW
I FGG SI HYFR VP REY WRDR LLK M KAC GLN TLT TYVP WNLH EPERG KFDFSG NLD LEAF VLMA
AEIGLW VILR PG PYIC SEM DLG GLP SWL LQDP GMRL RTTYKG FT EA VDLYFD HLM SRVV PLO
YKR GGPIIAV QVENE YGS YNK DPA YM P YVK ALE DRG IVE LLLT SDN KDG LSK GIV QGV LAT
INL QSTH ELQ LTT F LFNV QGT QPK MVMEY WTGF DS WGG PHN I LD S SEV LKT VSA IV DAGS
S IN LYMF HGG TNFG FMNG AMHF HDY KSD VT SYD YDA VL TEAG DYTA KYM KLR DFF GSIS GIP
L PPPPD L LPK MP YEP LTP VLY LS LWD ALK YL GE PI KSE K P IN MEN LPV NGNG QSF GY I LY
TSITSS GIL SGH VHD RGQ VFVN TVS I GFL DYK TTK I AVPLI QGYTV LR IL VENR GRV NYGEN
IDD QRK GLI GN LYLN D S PLK NF RI YSL DM KKS FF QRF GLD KWX SL PET PT L PAFF LG SLS IS
STPC DTF LKLEG WEKG VV FIN QNL GRY WNIGP QK TLYLP GPW LSS GIN QVIV FEET MAGPA
LQFTET PHL GRN QYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACCGGGAGCTGAGAGGCTCCGGGCTAGCTAGGTAGGGGTTGGACGGGTCAGGAC
CTGGTGGGGTTCTACTTGGCCTTCGGGGGCTAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTGGCCCGAGCCCCCAGGA CCTCATCTCCAATGTTGGAGGAATC
CGACACGTACGGCTGTCGCCGTCTAGACTAGAGGAGCGCTGTAACGCCATGGCTCCC
AAGAAGCTCTGCCCTCGTCCCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCTGAGCTGGATAAGGGGTCATGACCGGTTCTCCTAGACGGGCC
CGTTCCGCTATGTGTCAGCCTGAGCTACTTCCGGTACCGCGGGTGCTTTGGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGCTCAAGCCATACAGTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAACTGGCAGCCGGACCTCATGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCTGGGTTCTCGAAAACCTGAAATTCTAAGAACCTC
AGATCCAGACTCCTCTGCCGAGCTGGAACTCCTGGTCAAGGCTTGCTGCCAAGATATTC
CATGCCCTTATACAATGGGGCAACATCAATTAGCATTAGGTGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTTCCGTGACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACACTGAGATTGGCCAGCTGACAAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCAATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGGATTA
CTGGGCCAGAATCACTCCACGGCTGTGTCAGGTGAAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAAACATGACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGCTGCCGATAAGAAGGGACGCTTCCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTCTGGCTTCCGAGATGTCATCAGCAAGT
TCCAGGAAGTCTCTGGGACCTTACTCCCGGAAAGTGTGCTTGGGACCTGTG
ACTCTGCACTGGTTGGGACTTACTGGCTTCTCAAGGCTTGCTTGGCTTGGGCCCAT
TCATTCAATCTGCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATGACCCATACCTTGGACCAACACCATCTGGGTGCAAATAATGGAGTC
CATGAGCTGCCATGTGATGGTGGATGGGTGTTCCAGGGTGTGAGGAGAATATGGAG
AGACAAACATTTGGGAGGGAAACTGGGCTTCAACAGCAGTGAATTCAAGGGCTGTTGAACCCACATTCTG
GGAGGCTCAGCTGGGCTTAACAGCAGTGAATTCAAGGGCTGTTGAACCCACATTCTG
GGCAACAAACATCCCTAACCAAGTGGATGATGTTCCCTGAAATTGATAACCTGTGAAGTG
GTGGTCTCCCTCCAGTGGCAAATGGCCATATCTCAAGCTCTGGGCCACATTCT
ACTCCAAACATTTCAATTAGGCTCAGTGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCAACTCTGGATCAATGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCCCTAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGGCCAAGTCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAACTGGCACTTGAAGGTTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCAGCACTTGGGAGGCTGAGACGGGTGATTACCTGAGCTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCGTCCACTAAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAATCCAGCTATTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGGGTTGCAGTGAGTGGAGGTTGTAACACTGCACCTCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAA

FIGURE 66

MAPKKLSCRSLLLPLSLTLLPQADTRSFVVDRGHDFLLDGAPFRYVGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFGNSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWYGQNHSTRSVAVTKGLENMLKLGAJVNMVFHGGBTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMMML
GPVTLHLVGHLLAFLDLLCPRGPIHSISILPMTFEAVKQDHGFMLYRTYMTHTIPEPTPFWVPN
NGVHDRAYVMVGDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPPLKIDNLVKWWFPLQLPKWPYFQAPSGPTFYSKTFPILGSGVDTFLYL
PGWTKGQVWINGFNILGRYWTQKQGPQQTLVVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAAACACGTCTGCAAGCCCCAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTACACTCTCTGGTTATTCAGGATACCTTGAGGAATATT
CTTCGAAAAGTCAGAGAAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT
GCGTTCCCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAGAAATAAACTTAGGAAATTAGTTGAAACCATGAGTGGACATTG
AAAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGCTTGCACCTCACAGACCTGGATGTGCTAAAGCTTGA
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAAACAGACTGCTTAGTCTTGCCTGGGTGATTGCTCAAAA
TGCCTTACGTGAAGTTCACTGATGTTGCTGAAATTCTGCCTGGGTGATTGCTCAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCCGACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTTGCTCCACATCTAACAAAGTTAGTCATTCAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTTTTGCCTCTCAATTACAGGAACTGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAATCATCAGTTCCAGCATTAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTTATTCTCTAACAAACAAGCTCGAATCCTTACAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGAGCTAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCAATACTGGAAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAC
CTTGGACCGCCCTGCCAGGCCAGCTGGGGAGTGTGGATGCTCAAGAAAAGCAGGGCTTGGT
TGAAGATCACCTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTAAACTAAGATAATAATGCAAGTGTGAGCT
AACCTCCAGATTGCAAGTGCTCACGTACAAGTTTACAAGATAATGCATTTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGGTTAAAGTCATTCAATTCAAATCATTGTTTTCTTTGGGG
AAAGGGAAAGAAAAATTATAACTAATCTTGGTTCTTTAAATTGTTGAACTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCACTCGAAGTAAATGATTAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLS
VPDAVFDLTLDVLKLELIPEAKIPAKISQMTNQLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTTKLLVLNSLKKMMNVAELELQNCELERIPIHAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCGGCCTTCTCTGGACTTGCATTCCATTCTTTCTATTGACAAACTGACTTTTTATTTCT
TTTTTTCATCTCTGGGAGCTTGGAATCTTAGGCCGCCCTGGAAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGGTTCTCTCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTCGGGAGGGAGACCAGCTGG
GCTCAGTGCTTGCTTGCAACTATCTGCTTAGGACATCGAACTTGTGCTAGTGGCTCTGCTTACAGTGATTATGCTGTC
ATCGCTGGTGTATCCCTGGCCCTCTCTGCTGATAGTTGTGCTCTGCTTACCTCAAATACACAA
GCGCTAAAGCTGAAAGAACCTGAGCTGCTGCTGAAAAAATCACACCCAGACAAGGTGGTGGGCCAG
AACAGCCAGGCCAAACCAATTGCCCAGCTTGCTGCCAGTGCTGAGCTGGAGATAGAAATGTGTC
AGTTTGATTCCTGCCCCCTTGCTGACATAATAGGGCCCTTGAGITAGGAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGGCACCTGTTGTGATGTGCAAGGACAGAAAGGCACAG
CTCCCCCATCAGTTCATGAAAATCACTCAGTGCTGCCAGTGCTGGAGATCCCTACAGAGACTTC
CACTGGGCCAACCTTCCAGGAAGGACTTGCGAGAGAACCTCAGTGCTGGGAATGCTGATAAACCACTCA
CACAGCTGCTTATTCACACAAATCACCCCTGCTGGGAACTGACGTTTCCCTGGAGGTGTCAGAAA
GCTGATGTAACACAGAGCTTAAAGCTGCTCTTAAAGCTGCCAGGCCAGCTGGCAAGGAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCTCTTAAATTCTCTCTGTTGGCAGAGCTGACATGGGGAGGCTGAAGGCAAT
GCAAGCTGCAAGCTGAGCTAGGGGGTGCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTTGCACTTGCAAAATAGGAAAGACCAAAACAGCATCAGAAATTATCTTCTTCTATGTCAGCTT
GATCAGATGGAACTGTGAAAGTAAATTAAGCTTGCAAGGAACTTCAAGGATAAAACTAAACTTCAAAAGAGATTTCCTAGAAATAGAC
AAACAGTGGCAAATTGATTTCTGGCATCTGATGACGGCCCTCCACAAACTTGGCTGATTGGACAAGTCTG
GGCCGTGTACTCCCCACCTGCAATGTCATCAAACCTCTGCTGCTGTTCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTCCACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGTCTTCT
GACAGGATGAGAACTTATAAGCAAACTTCCATAGGGCTTAAACTCTGAACTCTGCAACAA
GACCCAAACTTGCAAGACAAAATATCAAATGTTGGAATTTCTGCTCTCTTAAATGGATGTTGACAATCAGA
AAAGTAGAGAGATCAGTAATTACTACACCAATAATCACCTTTCTGCTCATCTCAACTCTGAACTGATCACC
CGTCAGAAACAACTCCAGATTGTAAGTGTGAATGGACATAATTCTACAGTGGAGATAATACATAAAC
GAAGATGATGTAATACAAAGTCAAATGCACTGGCAAATAAACACAGCATGGCTCTTTGAAATCCAATTCA
TTGAAAAGACATACTTGAAATCACCATATTATGTAAGTTGAACCAAACCTTTTGTCAAGTTAGTCGAC
ACCTCAGATCCTAAATTGGGGTTCTTGATACCTGAGGCTCTCCACCTGACTTTGCACTCTCCAAAC
TACGACCTAATCAAGACTGGATGAGATGAAACTCTGTAAGGTGTATCTTAACTTGGACATATGGAGA
TTCCAGTTAATGCCCTTAAATCTTGAGAAGTATGAGCTGTGTATCTGCAAGTGTAAAGTTGATATGTGAT
ACCGATGACCAACAGCTCGCTGCAATCAAGGTGTGAAGGCAACAGACATTTCTCATATAAAATGG
AAAACAGATTCCATCATAGGACCAATTGCTGTAAGGAAAGGATCGAAGTCAGTGGCAATTGAGATTTCAGCAT
GAAACACATCGCGAAGGAAACTCCAAACAGCCTTCAACAGTGTGCACTGTGTTTCTCATGGTTCTAGCTG
AATCTGGTACTGTAGCGACAACTCAGTGAGGCAATTGTAATCACAGGGCAGACTACAAATACAGAAGCTG
CAGAACTATTAACCTAACAGGTCCAACCCCTAAGTGAGACATGTTCTCAGGATGCCAAAGGAATGCTACCTCGT
GGCTACACATATTATGAAATAATGAGGAAGGCCCTGAAAGTGCACACAGGCCCTGATGTA

FIGURE 70

MELVRRRLMPLTLLLILSCLAEELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPGSCESENIVFDTGTSNGPLLQVCNSKNDYVPFESSSSTLT
FQIVTDSARIQRTVVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTMSGLIGQVCGRVTPTFESSNSLTVVL
TDYANSYRGFSASAYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSAASTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVVIQSQNALGKYNTSMALFESENSEFKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPDSFASPTYDLIKSGCSRDETCVKVYPLFGHYGRFQFNFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYWKTDIIGPIRLKRDRSASGNMSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCGG
GGACATCGGGCCCCAGGAGCTCCCAGGCTCGCTTCCCGTGTGTTGCTGTC
TGCTGCCGCCGCCGTGCCACAGCGCCACGCCGCTTCGACCCCCACTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTCCTCGTCCCAGCTCGGTAGCAGTGGTCTGGTGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTAGTTCAAAATATGAAGAT
TTGGACCACTATTAAAGCAAAATTTTAATGCCAACAGTGGCAGATAATTTCAGGC
CTCTGGTCCAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGGT
CAGAATATTGGTGAACGTGGATGCCATAGATCAGGGGCCAAGGGGACATTGTCAAGGAA
CTTGAGGTAGGCCATTAGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTCTCCTGAGGATGAATCCAGTTACCCATAAGCGGAATTCCAG
TTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCTGAGGTTCTGTGG
TCGGATGGTGAACGGAGGACCCGATCAATCTGGAACAGCACAGGCTTCTGGCCTGGTT
ATAATGAAAGCCAGTTGGGGCACAGTGTACCATGTCACCATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGGCTCTATACCTGAGTGTATTAACCCAGGACATTTTGC
CATAAATGGGAAACTGCATGACAATAGACAAACTGCTCTGGGCTATAGGAGGAAAGCTGG
ATACTCTGACTATCTTACAATTGAGAATTGGTGAAGCAACTTGTAGAGACAGTTCTATGTG
GAGGAATCTTGTGATGAAATTGGGCCACACTAGGGCACCATTTCTGTAGTTTGAG
GAGCAGTGGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTCCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGCACAGCCACTTAACCTG
GATTCTTGGAGCAAATGGCATATTGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTCAGCAGAGTGGCTG
ATGCTGCAAGTTGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAATTATTGGCAGTTCAGCCCTTCCCTTTCCCACTA
AATTTCCTTAAATTACCCATGTAACCATTTAACTCTCCAGTGACTGCACTTGCCATTAAAGCT
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGTATTATGGACCGAATGAAAATTATTGTGAGGCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCACTGGTAGTCAT
TTTTTTTGTCACATCATAGAGTGTATTACAAATCCAGTGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AAATACTGTAGGCAATAGTAAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATAATGGTCACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAGTTGCTCTGGGTAGTCAGTGAAGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCAATTATAAACTAAGTGTACTGTAACCTTACAAACGTTTAATT
TTAAAACCTTTGGCTTTGTAAATAACACTTAGCTTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSCTLPELYELVNYYQPEVLWSGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSQLFLGHPKAILGATEVKLLGHGQPLNW
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCGGACTAGTTATTGAGCATCGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGTGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGTCTGGTCCAAGGCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGAGAATTATGGGGATCACCCCTGTGAGCAAAAGGGCAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTGCCGGCAAG
GACCAAGITGAACACAGCCTTGAAGACTAGGTTGAACACTTGCGAGCTATGGCTGGGTTGGAGA
TGAGTCGTTGTCATCTAGGATTAGGCCAACCCCCAAGTGTGGGAAAATGGGGTTGGTG
TCTGATTTGGAAAGGTTCCAGTGAGCCGACAGTTGCGAGCTATTGTTACAACATCTGAT
ACTTGGACTAACCTGTGATTCCAGAAATTATCACCAACAAAGATCCCATATTCACACTCA
AACTGCAACACAAACAACAGAATTATTGTGAGCTACACTCGGTGGCATCCCCCTT
ACTCTACAATACTGCCCTACTACTACCTCCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCACAGAAGTTTATGAAACTAGCACCATGTCACAGAAC
TGAACCATTGTTGAAATAAAGCAGCATTCAAGAATGAGCTGCTGGGTTGGAGGTGTC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGTCTGGATTGG
TATGTCAAAAGGTATGTGAGGCCCTTCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACAAAGTAGTAAGAGGAGGAAGGCCAATGAGTAGACCCCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAGAGTCCAAGTCCAGCAAACACTACCGTGCATGCCGG
GCTGAAGTTTAGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGGCAAAGAACAAAGAACAGTCCACCCCTT
GGTTCCAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAC
CCTCTCCCTTATGTAACCTGCTGGATCTATCCCTACCTCCAAAGGCTCCACGGCC
TTCTCTGGCTATGTCATAATATCCACTGGAGAAAGGAGTTTGCAAAGTGCA
GGACCTAAACATCTCATCAGTATCAGTGGTAAAAGGCCCTGGCTGTGAGGTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGTTCTACTGATTCCGAGCTCAGAC
CTTCTCTCAGCTCTGAAAGAGAAACAGTATCCCACCTGACATGCTCTGAGCCGGTA
AGAGCAAAGATGGCAGAAAAGTTGAGCCCTGAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTGTAAAGCTAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTAC
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAAACCTTTATAAAATTCTATTTTATCTGA
GTTCAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATAGTCAAGTGTGTGCAAGTATTACACTCTGAA
TGAATATTATTCTCAAAAATTGACACATAGTAGAACGCTATCTGGGAAGCTATTTCTCA
GTTTTGATTTCTAGCTTACTTCCAACAACTAATTTTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATATAACCTTAATTATTATTAAACATAACCTAAGAAG
TACATTGTTACCTCTATACCCAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA
GCCCTCTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTCAGACAAAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLLTSIWTRLLVQGSLRAEELS IQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGVGVLIWKPVSQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTOTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTTEVMETSTMSTETEPFVENKAASFNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFFFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLAEAV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATTGGTCCGCGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGCCCTGCTCTGCTGCCCTACTCGTAGGAA
ACTGGCCGCCGCTCTGCCACGGCTGCCACCCAACCGCGAAGACGGTAACCGTGTGACTTIG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCATAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCATCATTCGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTGGAAAGGTGGATGTTGGACGCTATACTGATGTTAGTACCGGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCTGTTCAAGGTGGCAA
GGAGGCAATGCGCGGCCAACAGATTGACAAGAAGGACGGGCTGTCATGGACCTCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAACTGAGCTATACCAGGGCCAAGAAAATATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGGCTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTTCTCCGTCAATT
CCAGGCTCTTCCATAACCACAGCCTGAGGCTGAGCCTTNNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGGCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCAAGCTGGGTAGTGTAACTGCTTATC
AGCTATTCAAGACATCTCATGGTTCTCCATGAAACTCTGTTGTTCATCATTCCCTTCA
TTGACCTGCACAGCTTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCCCCAAGGACTCTGCTTCAAGCCCTCTGGCTTGTATGGTC
TTCATTAAAAGTATAAGCTAACCTTGTGCGTAGTCTAACGGAGAACCTTAAACCACAAAG
TTTTATCATGAAAGACAATATTGAACAACCCCCCTATTTGTGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTTCCCTTGTGTGGTAGGACTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEEFFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

FIGURE 78

MGLLLVPLLLLPGSYGLPFYNGFYYNSANDQNLGNNGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPPVVPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTGCTACTGAGGCACGGGGCCCAGGGGAAGGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGCGGCCCTCTGAGCGACGCTCCCATGATGACGCCACGGAA
CTTCCAGTAGCACCATGAGGCTTCCTGGACGGAAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGACCGCATGGACCGCGGGGGAC
GGCGACGGCTGGTGTGCGCTGGCGAGCTCGCGCTGGATCGGCACACGCAGCAGCGGA
CATACGGGACTCGGTGAGCGCGGCCTGGGACAGTACGACACGGACCGCGACGGCGTGTGG
GTGGGAGGAGCTGCGCACGCCCTATGCCACTACGCGCCGGTGAAGAATTGAC
GTGGAGGATGCAAGAACCTACAAAAAGATGCTGGCTGGGACGAGCGCGTTCGGGTGGC
CGACCAAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG
AGTTCCCTCATGCGGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCAGGTGGAGGAGTACATCGCGATCTGTAUACTAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAAGCGAGAGGCAGCAGTCCGGACTTCGGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCGCC
CTGGTGGAAAGCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTGAGCAACCGCAGCTGCCACAGCCTCAGAGGCCCG
ACAATGACCGGAGGAGGGGGCGCTGGGTCTGGCCCTCCCTGTCAGGCCCGCAGGAG
GCAGATGCAGTCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCTGTCAACACCCCAACCCAGGGAGGGCTGTCAAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGGCCAGACCCAGGGACCCCTTGGCCAAGCTCAGCTCTAA
GAACCGCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCT
GGCCCGAGCCCTCTGCTGGCCTGCCCTGGGACACCTCCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAEIRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPQWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGGGAGCCCCGG
GCCGGCGGGCGGGGTGCGAGGGATCCCTGACGCCCTGTGCTCTGTTCTTTGTCGCTCCAG
CCTGTCCTGTCGCTTGGCCCCCCTCCCCCGGGTGCAGGGGTTGCACACCGATCTG
GGCTTCGCTCGATTTGCGCCGAGGCCCTCCCAGACTAGAGGGGGCTGGGCTGGAGCAG
CGGGTCGCTGTGCTCTCTCGCGCGGCCGGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACCGCGGGCCTCCGCACCCCTGGCCTTGCCCCGATTCTCCCTCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCGGCTCTCGGCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATG
TTTTACCAAGAGGTTGGACATCAGGAAGAGAAGAGCAGATGCTCTGCCAAGGGGCTGCC
CTCTTGAGGAATTCTGCTATGGGAACATAGTATACTGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGGAGTAATCAGCAACTCAGGGGACCTGACGAGTCTAGCCTAC
TGGTCGAGAAAATCTTCCAGTAGAGATGCCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCAGTAACAGGAAAGAGTACACAGGAGGCCACAGGACAAGCA
GTGCTCACAGCACATCCAACACAGGAAACAGGACTAAAGAACACCCGAGAAGAAAATCG
CAATAAGATTGTAAGCAGACATTGCAATTCTGATTGATGGAAAGCTTTAATTGGGCAGC
GCCGATTAAATTACAGAAGAATTGGGAAAGTGGCTCTAATGTTGGGAAATTGGAAACA
GAAGGACACATGGGGCTTGTCAAGCCAGTGAACATCCAAATAGAATTTCAGTGA
AAATTTACATCAGCAAAGATGTTGGTGTGCTAAAGGAAGTAGGTTTAGGGGTA
ATTCCAATACAGGAAAGCCTGAGCATCTGCTCACGGTAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCTCTGATGACAT
CGAGGAAGCAGGATTGTGCCAGAGAGAGTTGGTCAATGTATTATGTTCTGGCCA
AGCCTATCCCTGAAGAACATGGGATGGTCAAGGATGTCACATTGTTGGACAAGGCTGTCTG
CGGATAATGGCTTCTCTTACACATGCCAACATGGTTGGCACCACAAAATACGTA
GCCCTGGTACAGAACAGTGTGCACTCATGAAACAAATGATGTGCAAGAACCTGTTATAACT
CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTTGAATTGTTCTTCAACATAGCAAGACTTTGAAATCTGGCAGATTGGTGGCAAGAT
AGCTGCTGTACAGTTACTATGATCAGCGCACGGAGTTCAAGTTCACTGACTATAGC
AAAGAGAATGCTTAGCTGTCAAGAACATCGCTATATGAGTTGGAAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTTGGCTTCTATAAGGGAGGCCAACAGA
CTTCTAGTAATTGTCAGAGATGGGAGTCCTATGATGATGTCAAGGCCCTGAGCTGCTG
CACATGATGCAAGGAAATCACTATCTCTGTTGGTGTGGCTTGGCACCTCTGGATGACCTG
AAAGATATGGCTTAAACCGAAGGAGTCTCACGCTTTCTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCAGAGGATTGTTAGAGATTCTAGAACCCAGCAAAT
AATGGTAACATTTGACAACGTAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGATT
CTCATAATCTGAAATGTTAGCATACTAGAATCAGATAAAACTATTAAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCCTTAAGCCGCTGCCCTCTGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCAATAATCATGGCTTCAAGAAACTCAGGAAAGAGGA
GATAATGTCGATTAAAACCTTAAAGAGTTCAACCATGCCACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEAAPIAITCFTRGLDIRKEADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPFKKTGKDCKDIAFLIDGSFNIQRRFNLQKN
FVGKVALMLGIGTEGPVGLVQASEHPKIEFYLKNTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVIIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGETKYVKPLVQKLCTHEQMMCSKTCYNSVNIALI
DGSSSGVDSNFRLMELFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCGACCCGCGGGCCGCCACCGCGCCGCTCCGCATCTGACCCGAGCCC
GGCGGCCCTCCCGCGGGAGCGAGCAGATCCTCAGTCCGGCCCGCAGCGAACCTCGTCCAGTC
GGCGCGCGCTGCGGCCAGAGCGGAAGATGCGAGCGCTTGGGGCACCTGCTGTGCCAGTC
TGCTGGCGCGCGCTCCACGGCCCCCGCCTCCGAGCGACCTCAATGAGATGTTCCGCGA
GGTGAGGAACTGATGGAGGACACGAGCACAATTGCGCAGCGCGTGGAGAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGAAACTTACCTCCAGCTAT
ACAATGAGACCAACAGACAGAAGTTGAAATAATACCATCATGTGACCCGAGAAAT
TCACAAGATAACCAACACAGACTGGACAAATGGCTTTTCAAGAGACAGTTACATCTG
TGGGAGACAGAAGAAGGCAGAAGGAGGCCAGACTGCATCATCGAGGAGACTGGGGCCAGC
ATGTAUTGCCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGGGATGCT
CTGCACCCGGGAGCTGAGTGTGCTGGAGACAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACAGGGCAGCAATGGGACCATCTGTGACACACCAGAGGACTGCCAGCCGGGCTG
TGCTGTGCCCTTCAAGAGAGGCGCTGTGCTTCTGTGACACCCCTGCCGGAGGGCGA
GCTTGGCATACCCCCGCCAGCGGCTCTGACCTCATCAGCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCTGCGAGCCCCACAGCACAGCCTG
TGCTATGTCAGAAGCCGACCTCTGTGGGAGCGTGCACAAAGATGGGAGATCTGCTGCC
CAGAGAGGTCGGAGTGAAGTGGAGCTCATGGAGGAGGTGCGCCAGGAGCTG
AGGACCTGGAGAGGAGCCTGACTGAAGATGGCGTGGGGAGCTGCGGCTGCCCGCT
GCACTGCTGGAGGGAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTCAATAGAA
ATAGCTAATTATTTCCCAGGTGTTAGCGTGGCTTACAGGCTTCTGACAGCAGGCTTCTCCTACA
TCTCTTCCCAGTAAAGTCTCCAGGCTTCAAGCTGGCTTGTGGAGAGTGTGCAATTGTTCAAGC
TCCCCCAGGCTTCTCCAGGCTTCAAGCTGGCTTGTGGAGAGTGTGCAAGGGTTAAC
TGCAAGGAGCAGTTGCCACCCCTGTCAGATTGGCTGCTTGTGCTTACCAAGTTGGCA
ACAGCGTTGTTCTACATGGCTTATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAAATTTCACGCACTTCCATGGGCAAGGTAAGCTG
TGCCCTCAGCTGTGCAGATGAAATGTTCTGTCACCCCTGCAATTACATGTGTTTATTCTACCC
AGCAGTGTGCTCAGCTTACCTCTGTGCCAGGGCAGCATTTTCAATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGAGGGGTCATTGTTCTCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCT
CTGGTTGACTCTAACGCTAGTGTCTCCACTACCCCAACACAGCCTTGGTGCACCAA
AAAGTGTCCCCAAAAGGAAGGAGAATGGATTTTCTGAGGAGTGCACATGTGAAATAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTCTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT
TGCAATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGAGAAACAA
GTACTTAGGTTAATTGTAGGGCGAGGATTATAATGAAATTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACTGAGGAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCACTGCAACTGAACACTGACCTACGCCACTCCACAAATGATGTTTCAAGGTGCA
TGGACTGTTGCCACCATGATTGATCCAGAGTTCTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGTGAGTTAAATTATGATGATAACATAAGTTGCATTAGAAATCAAGC
ATAATTCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVTISVGDEEGRRSHECTIDECDGPSMYCQFASFQYTCQPCRQQRMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCACAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLQQNSNSIVRVDQSELGYLANLTELDSQNSFSNDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVAGMNLREISDYALEGLOSLESLSFYDNO
LARVPRRALEQVPGLKFLDLNKNPLQRVGPQDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDQLQRLPVREVPFREMTHCLPLISPRSFFPSLQ
VASGESMVLHCRALAEPEIYWVTPAGLRLTPAHGRRYRVYPEGTLELRRVTAEEAGLYT
CVAQNLVGDATKTVSVVGRALLQPGRDEGOGLELRVOETHPYHILLSWVTPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPSSGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

FIGURE 88

MRQTIIKVIKFILIICYTVYYVHNIFKFDVDCTVDIESLTGYRTYRAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRSSLKKYSFESIREESSYSIDPVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNNNEWTLKLDLQRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVТИPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIIEEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FPLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTGCCTGCTGCCGTGCTGGGCCTGAACGCAAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAACTTGGAGGAAATTGGGC
CCCTTGACAGTGATCTAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTAATGGTAGTGGTGCATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCCTGAAGACCTCTTCAGTTGCCCAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGACTCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCAGGGACCATCAAGTGCAACTTTGGGGGG
TGCCTTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCTCTCTGGGGACCTTACCTGT
ACAGCATGTCTCTCTCGAAGACAAAGGTCTGCAGAGGTGCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACTCTATAACATCTTAACTAAAGCACTCCCA
CGTCTACAAATGGAGTCGAGTCTAGAATTCACACAGGCCACCTAGTTGTCTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAAATTATTCCGAGGATCAATCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGGCCAGTCATTGCATTGAGGTGACGAGTTGCTGGAGGCAGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGTCAGGAGGCCTG
GGTCGGAAACTGAAGTGGCCAGAACTGCCTAATTCAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTCTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAAAACCTAAGATTTTAAAAAATTGGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTFGSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GТИКCNFAGVALGDSWISPVDVSLSWGPyLysMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNI LT KSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMLRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGGCGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCAATCACGTGCGCATCGTGGGTGGAGAGGAGCGCGAACCTGGGCGTTGGCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCTACTACACCCG
TTACTTGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACTAACACTAACACATCAGCCATCTGTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGCCAACGCCAACGGCGGAAGGATGCCTCGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCATTGAGTGGATCCAGAAC
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTTCTGTCTTGGTAAAAACACATCCAGTTGA
TGCCTTGAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSSLSSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTAKHIQPICLQASTFEFENRTDCWVTGWWYIKEDEALP
SPHTLQEVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDGGPLACNKNG
LWYQIGVVSWVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACACGGTCCGCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCCTAGGGCT
CTTTCGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGGAGCCCGACAGCGAGGAGACGC
TGCCCCCAGGGTGGCTCTGGGCCCTGGGCGGCCCTGGAGGAAGAGCTGAGTCACCTTT
GCCCTGAGACAGCAGAAATCTGAAAGACTCTCGGAGCTGGTCAAGGCTGTGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAAATGTGGCTGATCTGGTCAAGGCCATTCT
CACTGACCCCTCACCGTGCAAAAATGGCTCTTGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGTGGCTGAGCATCGACAAGCAGAGCTGCTGCTCCC
TGGGCTGAGTTCATCATATGTGGAGGACCTACGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAAGCTTCCACAGGGCTTGGGCCCCCATGTTGACTTTGTGGGACTGCAACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGACGCCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGTAACCCCCCTGTGATCCGTAAGCGATAACAACCTGACCTCACAGACGTGG
GCTCTGGCACAGCAATAACAGCCAAGGCTGTGCCAGTCTGGAGCAGTATTCCATGAC
TCAGACCTGGTCAGTTCATGCGCTCTCGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGACAACAGGGCCGGGGCGGGGATTGAGGGCAGTCTAGATGTGCAGT
ACCTGATGAGTGTGGTCCACATCTCACCTGGTCTACAGTAGGCCCTGGCCGGCATGAG
GGACAGGAGGCCCTTCCTGAGTGGCTCATGCTGTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGGACTCCCTCAGCAGGCCATACAGCAGGGTCA
ACACTGAGCTCATGAAAGGCTGGCCTGGGTCTCACCTGCTCTCGCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGGAAACACCAGTCGGCCCTACCTTCCCTGCCCTCAG
CCCTATGTCAACACAGTGGGAGGCACATCTTCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGGGTGGCTTCAGCAATGTGTTCCACGGCTTCATACCAGGAG
GAAGCTGTAACGAAGTCCCTGAGCTCAGGCCACATCCAGTTACTTCATG
CAGTGGCCGTGCTACCCAGATGTGGCTGACTTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATGGGTGCTGGGACCTCGGCCCTACTCCAGTGTGGGGATCCTA
TCCTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC
TGGGAACACCAACTTCCCACTTGCAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGTTGCTCCCTGCCCTGAAGCTGGCAGTTGAGTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGTCAGACAGCTTACTCCCTAACCCCTGAAA
TGCTGTGAGCTTGTGACTTGACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCCCTCAATAAGATGCTGTAACTAGCATTGGATGCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTTCCAAAGGGTTGTATAACAGACTCTGTGCACTA
TTCACTTGATATTCAATTCCCCAATTCACTGCAAGGGAGACCTCTACTGTCAACGTTTACTCT
TTCCCTACCTGACATCCAGAAACAAATGGCTCCAGTGCATACTTCATCTTGCTTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCTTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCACATTGAGATTGGCTCTCAGTTACTCATGTCCTGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
TGAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSFTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHVVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDEDLSSAYIQRVNTELMKAARGLTLFASGDAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPPIPWVSGTSASTPVFGGILSLINEHRLSG
RPPLGFNPRLYQQHGAGLFDVTRGCHESCLDDEVEVGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCTCCGGCGCCCACACCTGTCTGAGCGGCGCAGCGAGCCGGGCCGGC
GGGCTGCTGGCGCGGAACAGTGCTGGCATGGCAGGGATTCCAGGGCTCCTTCCCTCTC
TTCTTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTAACGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGCTGCTTGCCTCAGTCACCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTATAAGGAACT
CCACTGCCACTTACGAAGAGGCAAGCAATATCTGCTTATGAAACGCTCTATGCCATGG
CAGCCGACAGAGACGCAAGGGCATTCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGCAGATTATGGCTATGACAGC
AGGTTCAGCATTTTGGAAAGGACTTCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCTGGCAGAGAACGATGTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGAACCCAGAAGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTTCACTGGATCCGGTGAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCCTACCAAGCAATGCGATGCCAGGCCAGGGCCAGGGCTCTGGGTCTAT
GTGAGGATGTGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTCTGGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCACTGGCGTGCACACGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG
GTTTGTGTATCATATCATATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTTGGGCAATGAGGAATATTGACAATTAAAGTTATCTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTETQVGVIYILSSSGDGAQHRD
SGSSGKS
RKRKQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIHDGKTYVK
G TQKLRVGFLKPKFKDGGRGANDSTSAMP
EQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV
KDETYDLYQQCD
AQPGASGS
GVYV
RWMWKRQQQKWERKIIGIFSGHQ
WDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLD
DCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGTGGGGCTGTCTCGCACCTTCACCTCCCTGCTGCTGCTG
GGCTCGACAGCCATCCTCAATGCGGCCAGGATACTCTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCAGGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAACGGGACCCACCCTGCGCAGGTTCTGCTCACCAAGCCGTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGCTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGTGTGCTGGTGGAGC
CCCACCTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGTCTGCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTG
CCCACCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCCCTATGTGCCAGGTGGAGC
GGCGCTGGCTGCTGGCGGACATCATCAGCTGGGGCAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTGCAAGGGTGCA
GCTCCCGGGCGCCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCG
CCGCGCGCTCTAGGGCGCAGCGGGACCGCGGGCTCGGATCTGAAAGCGGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGGCGTTCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCCGGACGGCTGCTGGAAAGGAAACCCCCCTCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCTCATGCCCCGCCAAC
GACTTCCGGCCCCGGGGCCCCAGCGTTTGTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCGCCACATATCTTATTCTCCCAATTCAATAAAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVGSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTTSRWVITAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYWSKEGACADIALVRERSIQFSEVLPICLPPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALARAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCACCAATGCACGGCTCCTGCAGTTCCGTATGCTTCTGCTGCCACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGGCCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGTCACATGA
GATGGGACGAGGAGCTGGCGCCCTCGCCAAGGCCACGCACGGCAGTGCCTGGGGCCAC
AACAAAGGAGCGCGGGCGCCCGCGAGAAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCATGGAGGAGTGGACCACGAGCGTGAGCACTACAACCTCAGGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGGTATGGCCAAGACAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCGGGGAACTGTAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGTCCCACATGTCCCTCGGCTACCAACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCCGAAGATGTCAGGATTGCCCTACCTGGTACTGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGAAAATGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGCTGTGGAAACCCAGGC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGTAAAC
AACTGAGGTCCCTCCATTGGCAGCTCACGCCCTCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATGACCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTCTGGACCCCAAGATGCCCTGACAGGGCAAG
GGAACTCCTACCCCATGCCAGGAGGAGCTGAGGCTGAGGTGAGCTGCAGGCCACACTGGAC
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCTCAAGTCCCTGCCCAATTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTTGGCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGCTGAACTCGGGCCCTGGTATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCACTGCTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCTGCCCTCCCTCCCTGGAGTCTGGGGGTGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTGCCCACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTT
TTTGGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTCTGACTCTCAATAAAACCT
GTCCAACCTGTAAA

FIGURE 100

MHGSCSFMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVCWGHNKERGRRGENLFAITDEGMVDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVWWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTEVPSILAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTVPSRSPENSIDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGBHVGPPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLSDNLANTLVLKLNRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMBILOLDHNNLTEITKGWLGYGLLMLQELHLSONAIRISPDAWEFCQKLSLEDDLTNFNHLRSRLLDSSFLGLSLLNLTIHGNRNSYIADCAFRLSSLKTLDDLKNNEISWTIEDMNGAFSGLDKLRLIILQGNRIRSITKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGEVMEYTTILRLREVEFASEGKYQCVisNHFGSSYVKAKLTVNMLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVPEDDVFFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPQLNWTKDSPLVVTERHFFAAGNQLLIIIVDSDVSDAGKYTCEMSNTLCTERGNVRLSVIPTPTCDSQMTAPSLLLLDGWATGVVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSQQGTLADRDQGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGPMYLKGNVYGSDPFETYHTGCPDPRTVLMDHYEPSYIKKECYPCHSEESCRSFSNISWPShVRKLLNTSYSNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLGSEEDGKERTDFQEENHICTFKQTLENRYRTPNFQSYLDLT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGAAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG
AAGGATGCAAGCACGAGCTTCCTGGAAACCGAACGCAATGGATAAATCTGATTGTGCAAGAGAAGGAAGAAC
GAAGCTTTCTGTGACGCCCTGGATCTTAACACAATGTCTATATGTGACACAGGGAGCATTCAGAAATGAAA
TAAACCCAGACTTAGACCCCGGGGGTTGGTGTGTTCTGACATAAAATTAATCTTAAAGCAGCTGTTCCCCCTCC
CCACCCCCAAAAAAAGGATGATGGAATTAAGAACCGAGGATTCACAAAGAAAAAAAGTATGTTCATTTTCTC
TATAAGGAGAAAAGTGAACCAAGGAGATTTTGAATGAAAAGTGGGGCTTTTTAGTAAGTAAAGAAACT
GGTGTGTGTGTTCTCTTCTGAATTTCCCACAAGGAGAGGAAATTAAATAACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGAACCCGGCGAGGATTGAGGATTGAGGATTGGGGAGAGAACCGAGAGCAGATGG
TTTGCCCTATGTGACTAAATTCAGCGATAATTGAGATTGATTTCTCATCACACCTCTTTTTAAAT
TTTATTCTTCTTGTATCAAGATCATCGTTTCTCTGTTTAAACACCTGGATTTCCATCTGGATGTTGCT
GTGAGTACTGAAATACAACGTTGATTCAGAACAGGACAAACAGAGATAATTATGAAAGTGAACAAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGGACCCCCCTGTTGGTCT
GCTGGCTCTCACTTCTGTGTTGGCTGGTCGGTCTGGGGCTCAGACCTGCCCTCTGTCCTGAGCAA
CCAGTTCAGCAAGGTGATTGTGTTGGGGAAACCTCGTGTGAGGTTGGGATGCGATCTCCACCAACACGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAGTGAACACGCTTAAGCATTGAGGCACTTGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACATTGAAATTTGGGGCTTCAATTGTCGGCAACCTCAACACTCTGGA
ACTCTTGTGAACTTGTCTACTACATCCCAGATTGAGCTTTGATACTGCTTAAACTGAAGGAGCTCTGTT
GGAACAAACCCCCATTGAAAGCATCCCTCTTATGCTTAAACGAATTCTTGTGCCCCGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGTCACCTTGAGGATTTGAACACTG
CATGTGCAACCTTGGGAAATCCCTAACCCCTCACACCGCTCATAAACTAGATGAGCTGGATCTTCTGGGAATCA
TTATCTGCCATCAGGCCCTGGCTTCTTCAGGGTTGATGACCTTCAAAACTGTGGATGATACAGTCCAGAT
TCAACTGTGAACTGAGCAACCTTCACTTCAACTGAGCTTCAACTGAGGATCACCTGGCACACAATCTAAAC
ATTACTGCTCATGACCTCTTCACTCCCTGCTCATCTAGGGGATCATTTACATCACACACCTTGGACTG
TAATCTGTGACATCATGTGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACACAGCTGTGCCCCGTG
TAACACTCTCCCAATCTAAAGGGGACATGGAGCTGGGAGCTGCCAGAAATTCTCACATCTATGCTCTGG
GATTGTGGAGCCCCCTGAGACCTCAATGTCACTGAAGGAGTGGCGACTGAGCTGAAATGTCGGGCTCACA
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCTGACAAAGTGGGAGTACTGT
GCTCACTGTGAGCTGGTACGTTAAATTCTCACAAATCTAATCTGCAAGGATACAGGCACTGACACATGTG
TTCCGTTGGGAAATACTACTGCTTCAAGCCACCTGAAATTCTGAGCAACCTACTCTTCTTACTTT
AACCGTCACAGTAGAGACTATGGAAACGTCAGGGATGAGGCCGACGAGATAACAAATGTTGGTCCACTCC
AGTGGTGCAGTGGGAGGCCAACATGTGACCAACTCTCTCACACCCAGAGCAACAGGTGAGCAAGAAAACCTT
CACCATCCCGTGAACATGATATAAAACAGTGGGATCCAGGAATTGATGAGGCTGAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGTGTGCTGGTCTTCTACAAGATGAGGAAAGCAGCACCA
TCGGCAAAACCATCACGCCCAACAAAGGACTGTTGAATTATTAATGTGGATGATGAGGATTACGGGAGACAC
CATGGAAACCCACTGCCCATGCTCATGAGCATGAGCACAAATCACTACATCACAAATCTCCCT
CAACACACAAACAGTTAACAAATAATCAATACACAGTTAGTGCATGAAACGTTATGTGATCGAATGAA
CTCTAAAGACAATGTACAGAGACTCAAACTAAACATTTCAGAGTTACAAAAAAACAAATCAAAAAAA
GACAGTTTATTAACAAATGACACAAATGACTGGGCTAAATCTACTTTCAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTTATTAACAAATGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHEILQLSRNHIRTIEGAFNGLA
NLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNNAFDNLQSLVEINLAHNNTLLPHDLFTPPLHHLERIHLHHNPWNNCNDIL
WLSWWIKDMAPSNTACCACNTPPNLKGRYIGE LDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGN
TTASATLNVTAA TTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINV DDEITGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTTVNTINSIHSS
VHEPLLIRMN SKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRSLFIKASSMSHLQSLREVKLNNNELETIPNLGVPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELOTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRNRISSAIAPPKMFKLQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMELQLDHNNLTEITKGWLGYGLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDDSFLGLSLLNLTIGHGNRNRVSYIADCAFRLSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRISTKKAFTGLDALEHLLSDNAIMSLOQNAFSQM
KLQQLHLNTSSLCDCLQKWLQPQWVAENNQSFVNACAHQPLLKGRSIFAVSPDGFWCDDF
PKPQITVOPETQSAIKGSNLSFICSAASSSDSPMTFAKKDNEELHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISMHGSSYSVKAKLTVNMILPSFTKTPMDLTIRAGAMA
RLECAAVGHFAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCQAQNSA
GSISANATLTVLETPSFLRPLLRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPDPLVVTERHF
FAAGNQLLIIVDSVDSDAGKTYCENMSNTLGTERGNVRSLSVIPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWWVVIYHTRRNEDCSITNTDETNLPADIPSYLLSSQGTIADRQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFCPFLGSTGPMY
LKGNVYGSDFETYHTGCPDPRTVLMHYEPSYIKKKECYPCSHPSEESCRSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTGCGTCGGAGAGCCTTGAATGGAAGGCCGGAGCCGAGCTGAGAC
TGGGGAGCGCTTCGGCTGTGGCGCTCGGCCGGGGCGCAGCAGGGAAAGGGGAAGCTGTGGCTGC
CTGCTCCACGAGGGCACTGGTGTAAACGGGAGACCCCTGGTGGTCCCGTCCCTATCCCTCTTTATATA
GAAACCTTCCACACTGGAAAGGAGCGGGAGGAGGAGGGCATGGTGGAGCAAGGAGGAGGCCGCTGATCTGAG
GGCAGCACAGCATTGGAGCTTACAGATACCAAAATGAGGGAGGGAGGAGGAGAAGAACAGCTGCTGGT
TCACATCAGCCCTGGCGCCAGGGCATCTGAATCGCCACCCCCCTCGAGGCACCATGGCCAGAGCCGGTCTGC
TGCTCTGCTGCTGTGGCGCCACAGCTGACCTGGGACCTGTGCTTGCGGTGAGGGCCCAAGGATTGGCCGA
GTGGCGGCCACAGCTGAGGCCGAAGAACTTGTGGGAGGAGGGAGCCGGTGTGGTACTGAGCCCTGAGG
AGCCGGGCGCTGCCACCGCGTCACTGGCTGTGGAGGAGGGCTGTGAGCTGTG
GGGTATTGACCTGCGTAGTCTCCGGGGACTGCTGAGCACACCACCTATCTCTGAGAACAAACAGC
TGAAAAGATCTACCTCGAGGAGCTCTCCGGCTGAGGAGACTGAGGAGGAAACTGAAACCTGCAAAACAAACCGCTGA
CTTCCCAGGGCTCCCAGAGAAGGGCTTGGACATCTGAGAACCTCAATACCTGTACTTGGCCAATAAACAGC
TGACCTTGGCACCCGCTTCCCTGCAACAGCCGATCTGAGTGTGACTTGTGCGCAACTATCTCACCAAGATCT
ATGGGTCACCTTGGGAGAAGGCAAACCTGTGGGTCTGTGACTCTGCAACAAACAAGCTGGAGACGCCGG
TGGCGAACACATGTTCAACGGCTCAGCGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CCAAAGCACCTGCCCTGCCCTGTAACAGCTGACCTCAAGAACAAACAGCTGGAGAGATCCCCCGGGGCGT
TCAGCGAGGCTGAGCGAGCCCTGGAGCTTACCTCGAGAACAAACTACCTGACTGAGGAGGCGTGGACAACAGGA
CTTCTGAAAGCTCTCCAGGCTGGAGTACCTGTGAGGAGAACACACTGTCTCGGGTCCCAGCTGGGCTG
CGCCAGCTGGTGTGCTGAGGAGAACACGGCATCCGGAGCTGGAGGAGCAGGGCATCCACCCACTGGCTTCCAGGGC
GAGCCTGGAGTACCTGTGCTGACAGCAGAACAGCTGGGGAGCAGGGCATTCAGGAGTGTGCTGACCCCATCC
TCAAGCGTTGCAACAGGTGACCTGTACACAAACCGCTGGAGGCTGGCCAGTGGCTGCTGCCGCTG
GCAACCTCATGATCTGCAACACAGGATCACAGGATTGGCCGGAAAGTCTTCCCAACCTAATCTCTGGAGG
AGCTAACCTGAGTACACAGGATCACAGGCTGGCCACAGGCTGGCCACAGGCTGGCCCTTCCGAAGCTGGCCCTGTC
GCTGGCTGGACCTGTGGCGAACCGCTGCAACAGCTGGCACCTGGCTGGCTGAAATGTGATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTTGGCCAGGGGGCTGGGGCATGGCTAGCTGCGTGAAGCTGTGACTCTCA
CCAGCAACGACTGCGAGGCCCTGGGCCCTGGGGGGCTGGGGCATGGCTAGCTGCGTGAAGCTGTGACTCTCA
TCGCGGGGAATGAGCTCACAGAGATCCCCGAGGGCTTCCCGAGTCAGTGTGACTCTGAGTACCTGTGAC
AGATTAGTGGCTGGTGGAACTGGCTGGGGGGCTGGGGGGCTGGGGGGCTGGGGGGCTGGGGGGCTGGGGGG
TGGCTGGCTGGCTGGTGGAGCTGGCTTCCGGAGGGCTGAAGCAGCTGGGGGGCTGGGGGGCTGGGGGG
TAGAGTTGGTGCACATTCCAGGAGGGCTGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGGAAGGAGGAAACAGAATGAGTGCACAGGTGAGATGTGAGCTAGGATGAGTGTGAGCCGGGAGCTTCTG
AGCACAGCGCTGTGCTGTGAGGAGGGGGCTGGGGGGCTGGGGGGCTGGGGGGCTGGGGGGCTGGGGGG
TCCCATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCACGGCGACACATGC
ACACACATCACACCCCTAAACACCCAGCTAACACACACACACACACACACACACACACACACACACAC
CCCCACTACCGCTGCCACGCCCTGTAAATGTGAGGGAGGGCTGGCCCTGGCAACACAGGCACCCA
TTCCCTCCCCCTGTCAGATGTGATGCTGATGCAACACACACACACACATGCACAGTCATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTGCCCGAGGCAAAATGAGCTGGCCATAGCAGCTGCCGTG
GTCCATCTGCTCTGGCTGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GGAACTCACAAAGCTGGCTTTATTCCTTCCATCTATGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
TGGCCACCCCTGCTCTCCAGGTGGCTGGGAGTCACTCTGAGTGGGGAGGAGGAGGAGGAGGAGGAGG
CAGGGACTTCCAGTGGGAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CAGGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
GTTCTTCAGGGCTGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
CTCAAGAGCTGATTCTCTGTTAGAAAAACTAATATAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRLVLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFEEEPVILVSPPEEPGPGPAAVSCP RD CACS QEGVVD C G G I D L R E F P G D L P
EHTNHLSLQNQNQLEK I Y P E E L S R L H R L E T L N L Q N N R L T S R G L P E K A F E H L T N L N Y L Y L A N N K
L T L A P R F L P N A L I S V D F A A N Y L T K I Y G L T F G Q K P N L R S V Y L H N N K L A D A G L P D N M F N G S S N V
E V L L I L S S N F L R H V P K H L P A L Y K L H L K N N K L E K I P P G A F S E L S S L R E L Y L Q N N Y L T D E G L D N
E T F W K L S S L E Y L D L S S N N L S R V P A G L P R S L V L L H L E K N A I R S V D A N V L T P I R S L E Y L L H S N
Q L R E Q G I H P L A F Q G L K R L H T V H L Y N N A L E R V P S G L P R R V R T L M I L H N Q I T G I G R E D F A T T Y F
L E E L N L S Y N R I T S P Q V H R D A F R K L R L L S L D L S G N R L H T L P P G L P R N V H V L K V K R N E L A A L A
R G A L A G M A Q L R E L Y L T S N R L R S R A L G P R A W V D L A H L Q L L D I A G N Q L T E I P E G L P E S L E Y L Y L
Q N N K I S A V P A N A F D S T P N L K G I F L R F N K L A V G S V V D S A F R R L K H L Q V L D I E G N L E F G D I S K D
R G R L G K E K E E E E E E E E E E E T R

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCGGGCGCCGCAGCAGACCTGTCGGGCCGCGCCCTCGCGCTGTCTCCGGGAGCGGCAG
CACTAGCCGGCGCGAGGGCTGGGGCTTCCTCGAGACTCTAGAGGGCGCTCCCATCGGCCAACACCC
CAACCTGTTCTCGCGCCACTCGCTGCCAGGACCCCTECCCACATGGATTTCCTGGCGCTGGT
GCTGGTATCTCTCGCTACTTGAGGGCGCCCGAGGTTGACGGGAGGTGCCCCAGGAAATAGTGTATCGAT
TGGCTTAATGCTGTTATGGGAGGATTGACTCTGCTGGGCTGGCTGGCCAGTCTTGGGAGCAGTGTACGCC
TGTGTGCCAACACAGTCAAACATGGTGAATCTAGGGGAAACAAGTGCAGTGTATCTTGTTATGCTGG
AAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCGGCCCTGTAAGCACAGGTGATGAACACTTA
CGGCAGCTAACAACTGCTACTGCTCAACCGGATAATGCTCATGGCTGGTCTGGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACATGTCAGTATGCTGTGATGTGTTAAAGGACAATACTGGTGCAGTGCCTCCCTGGCT
GACCTGGCTCTGATGGGAGGACTGTGAGATGTTGCTACAGGAAGGAGCCTCTGCCCTAGATT
TAGGCAATGTCACACTTTGGAGCTTACATCTGCAAGTGTACAAAGGCTTGATCTGATCTGATTTAATGGAGG
CAAATAATCAATGTCATGACATAGGAATGCTACTTGTGAGTACAGTGCAGCAGCTTGTGATGTTATAA
CTAACCTGGGTCACAAAGTGCACAGGAAATGTAAGGAGGATACAGGGTGTGACTGACTTGTGATGTTATAA
AGTTATGATTGAAACCTTCAGGTCACATTCTGTCAGGAAATGGTACCCATTTAAAGGGTGACACAGGAAA
TAATAATTGATTCTCTGATGTTGAGACTTGTGCTGGCCTCGGAACACCATATTCTCTCATTAACCAA
CAGGCCACTTCTAACAGGCAACAAACAGGACTCACCAAAGGCAACACCAATTCTACTCCACCAACACCACCC
CTGCCAACAGAGCTCACACCTCTAACCCACTACACCCCAAGGGCAACACCCGGACTGACAACATTAGC
ACCAGCTGCCAGTACACCTCCAGGAGGATTACAGTTGACAACAGGTAACAGACAGACCCCTGAGAACCCAGGG
AGATGTGTCAGTTGCTGGTACACTTGTGACATTGAGCTTGTGATGTTGAGGAGAACAGCA
TGACTTGTGACTGGGAAACCAATCAGGGACCCAGCAGGTGGAACATATCTGACAGTGTGGCAGCCAAGGCCAGG
GGGAAAGCTGCAGCCTGGTGTACCTCTGCCGCGCTCATGCACTTGGGACCTGTGCTGTCACTCAGGCA
CAAGGTGACCTGGGCTGACTCTGCCACACTCCAGGTGTTTGAGGAAAACAGGTGCCCCACGGAGCAGCCCTGTG
GGGAAGAAATCTGGCTGGCCATGCTGGAGGAAACACAGATCACCTTGGCAGGGCTGACATCAAGAGGAATCA
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGAAATAAAGGAACCTGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGCAAAACCTTGTGTTCTGAGTATATGAGGGCAGAGAGGGTGGCGACAGAG
TCTCTCCATGTCACAAAGAACAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG
GCCCATTTGTTAGAATACTTCATAAAAAAAAGAAGTGTGAAATCTCAGTATCTCTCTTCTAAAGGAA
TAAAAATTGTCATTTAAGATGTTAAAGATGTTCTACCAAGGAAAAGTAACAAATTATAAGAATTTCACCA
AGATTTTGTGACTTACTAGTGTGAGTAACTTAAAGAACTTAAATTGGACAAGGCTTAATTAGG
CATTCCTCTGACCTCTAACGGGATTGAAAGGGGAAGGCCAACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCTCACAGTATTAAAGAAAAAGGAAACTTAAATCTAAAATGAGAGTATGTTGAC
AGATAATTGAGTCTCACAACTGCTCTGAGTTTCAAGATTTTTTAAAGAGATCTCAAGGAAACAGTTGAGAG
TTTCATTTGTCATGGATGATGTTGAGATTTTCAAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT
ATTTCATCGGGTCAATTCTCTCTGCTCTGCTGAGTGTGACAAGTATCTGGCTGCTGAGAAAGAGTGCCTGCC
ACACCCGTCAGACCTTCTCTCACCTCATGAGTATGTTCTCTTCTTCAATTGGACTCTCCAGGGTCC
AGAACAGTAATATTGGAAACAAATAGGTACAATAGAAGGTCTCTGTCATTAACTCTGTTAAAGGCAGGGCTG
AGGGGAAATAAATCATTAAGGCTTGTGAGTAACGGCAGAATATGGCTGAGATCCATTGTTAATGGTTCAIT
TCTCTTATGTCATATACTGCACAGCTGAAGATGAAAGGGAAAATAAATGAAATTTTACTTTCTGATGCCAA
TGATACTGCACTAAACTGATGGAAGAAGTTACCAAGTACTGTATAACATCTGTTTATTATTAATGTTT
CTAAAATAAAAATGTTAGGGTTTCAAATGCCATAAAACAAATTGTAACAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVQCQ
RCKHGEC1GPNKCKCHPGYAGKTCNQDLNECGLKPRPCPKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSY1CKCHKGFDLMDYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVY1PKVMIEPSGP1HVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPOKPRGDVFSLVHSCNFDHGLCGWIKEKDNDLHWEPIRDPAQQYLTVAAKAPGG
KAARLVLPLGLRMHSGLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSEQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCACAGGTGCTTGTGGGGCTGA
AGGTGACAGTGCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCCTACCTACCGCTA
CACTATGGCTTCAACACTCCAGCATCACAGATCATGGTATTGAGAGACCCCA
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGTGACTTGGAAATACC
AACACAAGTTACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTCCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACTCTATCTGCCAGTCA
GAAGATACAAGTCACGGTGTGATCTGTCAACAGGAGCTGGTCAGATTCTCCTCC
CTGGGCTGTGGAGTGTGGGAAATGACCCCTGACATGCCATGTGGAGGGGGACTCGG
CTAGCTTACCAATGGCTAAAAAATGGAGACCTGTCCACACCACTGCTCCACCTACTCCTTTCT
TCCCCAAAACAATACCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCCTGTTGAGGAACCTGTCAGTGAATGGAAAGTGTATCATTTATGCCCATCATATATTAT
GGACCTTATGGACTTCACAGTGAATTCTGTATAAGGGCTAAAGTGGGAAAGTGTAACTGT
TGACCTTGGAGAGGCCATCTTGTGATTTCTGTGCTGATTCTCATCCCCCAAACCTACT
CCTGGATTAGGGAGGACTGACAATACATATATCATTAAGCATGGCCTGCTTGAAGATTT
GCATCTGAGAAAGTACCCCAGAAGACAATGGACTATGTGTGCTGTTACAACAAACATAAC
CGGCAAGGCAAGATGAAACTCATTTACAGTTATCATCACTCCGCTAGGACTGGAGAAGCTTGT
CACAGAAAAGGAAATCATTGTCACCTTCTGTGAACTAAACTGGAAATCATTTTGATT
ATATCCTATGTCCTCTCTCATGGAAAATATCAACCTTACAAAGTTATAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAACATACAGGAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTCTTCAGG
ATTCCAAGCAGGTCTGTCAGGCCCTGTATTGTATCGGGAAGATTGACAGTACAGT
GTATGAAGTTTACAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAATTCTCATGG
GCTAAACAGTACATTGCTAGTGAATTTCTGAAGAAACATTITAAGGAAACACTGGAAAAGT
ATATTAATCTGGAAATCAGTGAAGAAACAGGACCAACACCTTACTCATTATCCTTACA
TGCAGAAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGCTT
GTGCAACAGAAAATCAGTGGGAAATATTCTCAGTGGAGACTCTCTCATGCTGACGGC
GGAGAACAGGAAAGTGCAGGGTTCTCATAAAGTTGTATGAAATATCTCATACAAACCTCA
ATTAGTTCTACTCTACATTCTACTCATCACAAACTGAGACTATCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTGTTATTAAATTTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTTGTCACAAAAACAAAACACTGCTCTCTTCTTCAACCTC
AGTAGTATTGTTGAGAAGACTGTGTAACCTTAAGGAAATGACTTAAAGTCTTATT
TTTTTCAGGAAAGTGGATTCAAATAATTATTCTGTTTGTCTTAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPNASLLINPLQFPDEGYIIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNTMLTCHVEGGTRILAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIICKHGPRLLEVASEKVAQKTMVDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCGGGAGTCTTCAGTTCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCTCCCTGGACGCAGGGCGGCCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACGCTGGAAAGGAGACTGGATGATAGATAGATTTTATGCCCGTGGCTGC
TGTCAAAAATCTTCACCGGAATGGCAAAGTAGTTTGTCAATGGGAGAAGATCTTGAGGTTAA
TATTCGCAAAGTAGATGTCACAGAGCAGGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAAAGATGGTAATTAGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTATAAGTGTAAAGAGTGGAAAGGACTATGAGCCGTTTATCATG
GTTGGTCCAGGTTCTGTCTGAGTAGTATGTCAGCACTTTCAGCTATCATGTGGA
TCAGGACGTCGCATAACTACTTTATTGAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGACTGTTATTAGGACTCTGTATGATAATTGTC
AGATTGCTTGTCTTCAAAAGGCGCAGACCACAGCCATACCCATACCCCTAA
TATTATCAGAATCTGCACAACCTTGA
AAAAAAGTGGAGGAGGACAAGAGGCGGATGAGA
GATGTTCAGAAGAAGAAGCTGAAAGAAGGAAACAAAGACTTCCACAGAATGC
CATAAAGAACACGCTCTGGGCCATCATTGGCCACAGATAAATCTAGTTAAATTAG
TTATCTTAAATATTATGATTTGATAAAACAGAAGATTGATCATTGTTGTTGAGTG
AACTGTACTTTTGAAATATTGCA
GGGTTCAGTCAGTCTAGATTGTCTAAAGTTGAAATATGATTTAAGCACAGTGTG
GTTTAAATATTCTCTAA
TTTCAAGTCTGAGTTGAA
AAATTTCAAGTCTGAGTTGAAATTTACATTCCCAGTATTGATTGATTGATT
TTAAATTAACACATTTCA
TTTCAAGTCTGAGTTGAAATTTACATTCCCAGTATTGATTGATTGATT
TGAGGTTTTAAGAAGATTAGAGAAAATATTCTCATTGATATAATTCTCTG
TTTCACTGTGAGAAAAGAAGATATTCCCATAAATGGAAAGTTGCCATTGTC
AAATGTATTTCAGTGACAAATTCCGTTCTTTAGAGGTATTTCCAA
ATTTTTCAAGGTTATGCAACTAAACACATTTCAATTAAATTACAGTTCTACACA
TGGTAATTACAGGATATGCTACTGATTAGAAGTTTAAAGTTCACTGGTATTCTCTGATTC
CAACAAAGTTGATTCTCTGTATTCTTACTTACTATGGGTACATTTTTATTTT
CAAATTGGATGATAATTCTTGAAACATTTTTATGTTTAGTAAACAGTATT
GTTTTTCAACTGAGTTACTGAGAGATCCATCAAATTGAAACATCTGTTGTAATT
TTGGCCCACTTTTCAAGTTTACATTCTGCTGAACTTCAACTTGAAATTGTTTTT
TTTCTTTTGAGATGTGAAGGTGAACATTCTGATTGTTGCTGTGAAAGCCTGGTA
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCTACTCAGGAAAAG
CATCTTCTTGATATGCTTAAATGTAATTGCTCTCATACAGAAAGTTCTTAATTGAT
TTTAACAGTCTGTAATGCTGATGTTAAAATAATAACATTTTATTTTAAAGACAA
ACTTTCAATTATCCTGTTCTTCTGACTGGTAATATTGTTGCTGGAATTCCATTAGATTACAG
GTCAGTAGGATGGAACATTAGTGTATTTTACTCCTTAAGAGCTAGAATACAGTTT
CACCTTAAAGAAGGGGAAATCATAAATACAATGAACTGACCATTACGTAGTAGAC
AATTTCCTGTAATGCCCCCTCTTCTAGGCTCTGTTGCTGTAATCCATTAGATTACAG
TATCGTAATATAACAGTTTCTTAAAGCCCTCTCTTGAATTAAATTTGACCATT
AAAGAGTTGGATGTGTACTTGATGCCCTAGAAAAATCTTAAGCACAAAACCT
TTCTAACCACTTCATTAAGCTGAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRPQPYPYPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEEALTSKAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQR OFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEG DYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTTRLLSLDP SHERAGGNLR
YEQQLLEEREREKTLTNQTAELATPEGIYERPVVDYLPERDVYESLCRGEGVKLTPRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHI VRYYDVM SDEEIERIKEIAKP K LARATVRDPKTG
VLTVA SYRVSKSSWLEEDDPVVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDF S
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDILGAAIWPKKGTAVF WYNLLRSGE GDY R
TRHAACPVLVGCKWVSNKWF HERGQEFLRPCGSTEV D

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270, 346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TCATTTTACCGTCTGGCTGGGTTAGTCCGACACCTTCAGTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGAAACATCTCTGGGATGCTGCTCTGAAAGCAGGGGCCCTGCTCTGCTCTTGGCCTCATGGACCC
CAGGTTCTCTGGTTAAACTGAAAGCCTACTGGCTGGCTCCCATACTCAATTGATCTTGAGGCTGTGCC
CTGGGGCACCCACCTGGCAGGGCTTACCCACATGCGACTGAGCTCCTGGGTTCTGAGTACAGGGGAGGGAGAAG
ATCCCTGTGAGGCTGTAGGGAGCAGGGGCCACAGAAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAAACCCCGGATTGCTCCCTACTACAGGGCCACAGAACTTCAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCGGTGGCGTGGCTGAGCGGTTCTGCTGACCTCCAGACTACTGTCCA
CTTGCCGCTGGCTGTGAACCGTAGGGTGCCCCATACTTCCCTGGTTACTCTACTTCACTGGCAGGGGG
CCGGGCTCCAGCAGGGATGAGCTGGGATCTCATGGGATGAGCTGGGCTGGCTCATGAGACACATATGCGAGGCC
GCCACCTTCACACACTTGGGGCAGACTACAGCTTCATCATGAGACACATATGCGAGGCC
CCGGCCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACTGTACTTGGGCTGGCTCATGAGGAGTCTCCTGCTGC
GGCAGGGCAGCAGGGCGTACTGTGAGGGCTTGGACTACTTACAGGCGCTGGCTGAGGCTTGGAGCTGCCATTG
GCCACATCTGGATGGCTGGCAGGAGACATTCTCAGTGGGGCTTGAGCTGGGCTTGGAGCTGCCATTG
ACTCTCTGGCGCTGCGCTGTCTCACACCAAGGGCAGCAGTATCGCTCATTTGAACCTGGCCAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGGCTTCCGGTGGACCCCTGCTCGAGGTAACCTCATGT
ACCGGCTTCACAAACCTTCAGCGCTCTGGAGTTGGACGGGCTTACAGTAAATAGAACAAACTCAGGCTCAGA
TCCGGAACCTGACCGTGCTGACCCCCGAGGGAGGAGCAGGGCTGAGCTGGCCGTTGGGCTCCCTGCTCTTCA
CACACACACTTGGGCTTGGAGGCTGAGGGCTGAGGACTACTTACAGAGCAGCACACCTTCTCTGAGATGGGG
CTTCCAGGTGCCACTACAGGGGCTAGAGGGGGAGCTGGGTGATGGTGTGGAGACTGCGCTGGAGCAGCTCA
ATGGCGCTATCACGGCCCGCTGGCTTCCAGAACGAGCAGGCTGCTCACCGCTATGGGCGCTTGAGCCAGCAC
GGGGCATGGAGTACACCCCTGGAGCTGCTGAGTGGAACTGGGCTGGGCTGGACCCCTGGCTCGA
GGGTCACTGGCTCTGGGGCACTGAGGGTGGAAATCTACCTATGCCCTATGTCACTGAGGGCACCCAGTGC
AGCTGGTGTGGCTTCCAGGGCTGAGCTGCTGAGGCTGGCTTCCCTGGAGGGCTTGGCTGAGCCAAATGTC
TGGAGGACAGAGAACATGAGCTGGCTGAGGGCTGAGGCTGAGGCTGAGGAGTGGCTGGAGCTGGCTGGCTCG
ACCCCAATTCTGGGGTGAAGGCTCAGAGGGGCTAGAGGGCTGAGGAGTGGCTGGAGGAGTGGCTGGCTGGCTCG
CTGTGAGGAGCAAGGGCCCTTCCAGGTGGCAACTCATGGACGTGGCTCGAGAAAGCACCCCTGGAGACTCT
TCTTCTTACACCGCTGGACAAGGGCTGGGGCAACTCTCAACCGCTGCGCATGAAATGCCATCTCTGGT
GCCAGGGCTTCTTCCAGTCATTCAGGAGTCAATCTGCCCTGTCACACAGAGATACCCAGGGGCC
CGGGGGCTGGCCCTGACCCCCCTCCCTCTGGCTGAGGCTGGCTGAGGCTGGGGCTTCTATAGGGGGAGATTG
ACCGGCAGGGCTTCTGGGGAGGGCTGCTCTACACAGCTGACTACACTGGGGCCGAGGCGCTGGCAGGTGAAC
TGGCAGGGCAGGAAGAGGGAGGAAGGCGCTGGAGGGCTGGAGGTGATGGATGGATTTCTCTGGTCTCAGGGCTCC
ACCTCTTCTGGGGCTGAGGAGGGCTGGAGGAGGAGGCTGGAGGAGTGGAGCAGGCCACGGCTCAGTGAAG
AACTCTACACCGCTGGCTCAGCAACTGGAGGGCTAGGGGGCTGGCCAGCTGGCTATGGCTCTTGT
AGCAGGGAGCAGGCAATAGCACTAGCCGCTGGGGCCCTAACCTCATACCTTCTTGTCTGCCAG
CCAGGAAGGGCAAGGCAAGATGGAGCAGATAAGAAATTGTTGTGATTTTAAATATGAAATGTTAA
ACATGTCCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSSRARILD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVANRTV
AHHFPRLLYFTQORGARAPAGMQVVSHGDERPAWIMSETLRHLHFTFGADYDWFFIMQDDTY
VQAPRILAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLRSRSLLLRPHLDGCRC
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTLDDLLECVTQRGHRRALARRVSSLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAAANVLEPREHALLTLLLVYGPREGGGRGAPDPFLGVKAEEELEERRYPG
TRLAWLAVRAEAPSQVRIMDVSVSKHPVDTLFFLTWTRPGPEVLRNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGFRFDQASAEGCFYNADYLAA
RARLAGELAGQEEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGGLGGRAQALAMALFEQEQQNST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~G~~CCAACGTGAGAGGAACCCGTGCGCGCTGCGCTTCCTGTCCCCAAGCC
GTTCTAGACGCCGGAAAAATGCTTCTGAAAGCAGCTCTTTGAAGGGTGTGATGCTTGG
AAGCATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCA~~T~~GAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGAGTAAGGAGACTTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTCTGAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACA~~A~~CTG
GTTCTCCTGCACGCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGTATGAAAGGAGGAATTGCTTAAGTGTAGAATCAATGAAAAGACTTAAAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGTTGGAAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGAGAAGATGCTGATGGA
AAAGATGTATTAAACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTAGATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTTACCGCCTTAGGGCATTTGGCATTTCAAT
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGAGTAGTAACTACATATCCAA
TACAGCTGTATGTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTAAATGAGGGTGGTTCTTCTTAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAATTCTAAATTATGAAACATTAGAAATCTGGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTCTAAGATATGCAAATGATCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTAGCTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCAAGTCCAATGGATTGCCTCTCAAAATGTACAACAGCAACTAAAGAAA
ATTAAAGTGAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVLAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHI FNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGCGTCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAAACACAATGCACAGAGAGAGGATGCTTCTCTCCAAATGTTCTTATGAACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCTGTTCATCACAGATGTGTTGACATTTCGCAT
CTTTCAAAACCTGTGATGAGAAAAAGTTCACTGAGAATTTCACAGAGCTCTGCT
ACAATTATGGATCAGGTTCACTGAGAATTGTTGTCATTGAACGGAAATTTCATCC
AGCTGCTACTCTTTCTACTGACACCATTCCCTGGCGTTAACGTTAAAGAAGCTGTCAGC
CATGGGGCTCACCTGGGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTACAAGA
AACCTAAAATGAGAGAGTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAAGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGCCAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAAACCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTCGGATTTGTGAAATGGTAGGAATAATCCTTG
AAACAAAGGAAAATCTCTTAAGAACAGAAGGCACAACTCAAATGTGTAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACAGAGAAATTGTCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATAACAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLLWTAGIPIFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWVDTGPTLTKSLSFWDVGEPPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGSLSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCGCTGCCGCTGCCCTCAGAACCCCTGACATGGCGCTGAGGCCGACCCGGAC
TCGGCCTCGGCCCTCGCTGCCTGACTTCTCCCTGCTGCTGCTGCTTCAAGGGCTGCCGTAGGGCTGTAAATC
TCAAAATCCAGAACATTGAAACCCAGTGGTACGAGATTGAAAGTGTGAACTCTCTGCATCATTCAGGATCTGC
AGACAAGTGACCCCAAGGATCGAGTGAAGAAAATTCAGAGTGAACAAACACATACTGTGTTTTGACAAACAAA
TTCAAGGGAGACTTGGCTGCTGAGAAGAAATCTGGAAAGACATCCTGGAAGATGTGGACAGCAGAG
ACTCAGGCTTATCGCTGGTGGAGTCCTGCTCAAATGACCCCAAGGAAATTGTAGAGATGTGATCAGGTTAA
CTGTGCAAGTGAAGCCAGTGAACCCCTGTCAGTGAAGTGGCCAAGGCTGTACCAAGTAGGCAAGATGCCAAACTG
ACTCGGAGGAGTGAAGGGCCACCCCGGCCCTACACTACAGTGTGCTGAGTCACTGGCCACCCAGGATT
CCAGGACCAATTCCAGATTCTGCATTCCTTCCTCACTTAAACTCTGAAACAGGACTTGTGCTGACTCTG
TTCAAGGGAGACTCTGGCAGTACTACTGCTCATGGCTCAATGACGCCAGGCTCAGCCAGGTGAGGAGCAGG
AGATGGAAGTCTATGACCTAACATGGGCAATTATGGGGGHTCTGTTGCTCTGCTGTACTGGCCCTGA
TCAGCTGGGATCTGCTGTCATCACAGCCGGTACTCTCAACAAATAACAGGATGGAAAGATTCAGA
ACCCAGGAAACAGATGGAGTTAACATCACCTCGCACTGACGAGGAGGGCAGTTCAGACACAAGTCTCGTTG
TGATCTGAGACCCGGCTGTGGCTGAGGCCACAGAGCCACCTGCACTAACCTCTGCTGTAAGAAACTCTGCTCAA
GCCAGGAGAGTGTGACTGCCAGACAGTACAGACACTCATCTTCAAGGACTTCTGGCCAAAGTGTGACCA
CTACTCTCTACTCTAACAAAGCCACATGAATAAGAAGATTTCCTCAAGATGGACCCGTTAAATAACACAA
GGAAAGGCAAACTGGGTCGCTGACTGAGTGGGCTCTAATCTGTTCTGCTGATCCCCCTAGTGAATTAG
TGATCTTAAAGAGTTGCTCACGTAACCCGGCTGTGGGCTGTGGAGGCTGATTTAGCTTCAACCTGGCTG
CAGCAGCCACGACAGCACCAGTGTGAGATGGCGAGGTGGCTGGCAGCACCAGCAGCGCATCCGGCGGAACCA
GAAAAGGCTTCTTCAAGGAGCAGCTTACTCTCATCGGCCAACAGACACCAGCAGGCTTCTTAAAGGCTG
TGATCTGGTGTGGCTGAGTGTCCATGTTGGAGAATTTGGATCAGCATTTTGCTTAAACAAACAAAAATCAGGAA
GTAATTGGTGTGGAAGAGGGATCTGGCTGAGAACCTGTTGTCACAGGGTGTAGGATTTAAGGAAA
ACCTCTGCTTAAAGGCTGAGTGTGAAATGGTACTGAAATGGTCTGTTCTGTTCTGTTTAAATAAATT
TACATCTTAAATTGCTAACAGGATTTGATTTGATTTGATTTGAAAGAAAATTCTTATTAAACTCTTAA
CATACATGTTAAATAACCTATTTCCTTAAAGGTTAACCTAACCTAACCTAACCTAACCTAACCTAACCT
TGGAAGGAAATCTAAATAAAGGTTTACCTTACCAAGGAACTCTCTCATGGAGTTTACTCTGATGTTCTTCTT
CACACAGATTCTTGGCTTTTCAAGGAACTCATACTGTCATCACATCAGGACATTGTTGAACTGAAACCT
TAAATTCTCAGTTAACGATGTTGAAATCAGTTGCTCATCTCTTAAAGAACCTCTCAGGTTAGCTTGAAC
GCTCTTCTCAGGACTGAGACTGAGACACTGCTAACCCAGGCCACCCAGCAGGCTTCTAGATCACACAGAT
CCAGTGTGCTGGGTTGGGCCAGGCCAGGCCCTCTAGTCACTGTGCTCTGCTGCTGCTGCTG
GCCATCTGGGCCCTGGCAGTGGCTGTCAGTGAGCTTACTCACGTGCCCTTGCTCATCAGCACAGC
CTCTCAGGTGGCAGCTCAGGACACTGGGACTCTGGCTCTCCATGTCAGGCCCTGGCTCTGTAACAGACCT
CTTGTGTTATGGCTTACAAAATAGGGCCCTTACAGTCTTAAAGGTTGTTTAAAGTTGTTTAATTATTGTT
AAGATTGCTAAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAGTACAATAAACATTTTAAAGAAAATGGAT
CCCAGTGTGCTTCTTGTGCAAGGAAAGCACCCAGGCCACAGGCTCTGCTGCAATTCAACAAACACCATG
GGAGTGGCCGGCAGCTCAGGCTTTTAAAGAACGTCAGGTGGAGCAGGCCAGGTAAAGGCTGCCGGAGGAAG
TGAAACCCCTGAAATCAAAGCAGTTTCTAATTGACTTTAATTCTCATGGCCGAGACACTGCTCCATT
TGTGGGGGGAGCATCTGACAACTCATCGAGAACGGCTGTGTTCTCAAGGAGCAGGTTCTCAGCTTACATG
GCCGCTGCTGGACTCAGGACTCTGAAAGCAGGACTCTGAGAAGGAGCAGTCTCACTGCTGCTG
GAATGGCTCTCACTACTCACCTGCTTCAAGTCTGTTCTGAGTCTGTTGGGTTTTTAACTCTTGTACAG
AATTGCTACATGAGACTGTGTTGACTTTTGTGATTGATGAAACACTTGGCCGAGGCCCTGGCAGGAG
GGAATGCTCAGGACTGGCTCAGTGTCTCCCTGGTGTGCTGAGTGTGCTTCACTGGTCAATTGCT
CCTCCATCATGCCCACCTTGGTAGAGGAGATGGCTCCACCCACCTCAGGGTTGGGATTCACTGGCTCAGC
TCTGGTGTGCTAGTGTAGGGTGCTGCTTCTGCTTCAAGGAGACTGAAAGTGTGCTGCTTCAACTGAG
TGGCAACAGGCTGCTTAAAGAATGAGAGAAGTGAAGAATGGAGCTGAGTGTGCTTCAACTGAGACTAGA
CGGAAAGGAACTACTCTGTTAAAGATGATGAACTGACTCAAGACTCGAGGCCGATACAGGCTGTGATTCT
GCCCTTGGGATGGTGTGCTGACAGATGCTACAGACTGACTAACACCCGTAATTGGCATTGTTAA
CTTCAATTAAAGCTTCAAAACACCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRICARLPDFFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTCPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHILNSETGTLVFTAVHKDDSGQQYYCIASNDAKSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267